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AV241667 XM777111.X
A1772957 EST254057
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AW648529 EST326983
BB571653 BB571653
BH273274 CH230-23H
                                                                                                                                                                            A1991076 wu36fil.x
BE36692 PIL 42_C1
AQ004063 CIT-HSP-2
A103567 mo25dil.r
E8367090 PIL 42_C1
A1668111 TENGG1036
B56693 CIT-HSP-581
A1054920 coaug0021
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A0957276 LERAOBGTR
BM943047 UL-M-EQO-
BM947057 UL-M-EUO-
BC443079 UL-M-EVO-
ACT49010 HS_5575_A
BO941497 AGENCOURT
BM484625 53845 MA
AACT8411 PG3811 C
SF4611573 UL-M-CGOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 bp mRNA linear EST 16-JAN-2001
PM4-EN0068-151100-004-b06 EN0068 Homo sapiens cDNA, mRNA sequence.
BF849816.1 GI:12236966
BFR49815.1 GI:12236966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 535)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
AW855235 RC1-CT028
BR512001 BB612001
BB613951 BB613951
BB617396 BB617396
BF601265 266197 MA
BG991167 MR2-HT118
                                                                  AA910328 Ok83c11.s
AI744019 wc32g02.x
AI793020 qz39a03.y
AI373743 qz54c04.x
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AV361506 AV361506
AW5.16927 xp88h07.x
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20020663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwing Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
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 AW856235
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BB613951
BB617396
BF601265
BG991167
                                                                  AA910328
AI744019
AI774019
AW241667
AW241667
AM772957
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AW648529
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BH273274
AI91076
AG04063
AA103567
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AQ957276
BM9637057
BM947057
BQ443279
AQ749010
BQ941497
BM64625
AA078411
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  RESULT 1
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                         (without alignments)
18293.095 Million cell updates/sec
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                                                                                                                                              1 gacagtgttcgcggctgcac......tgtccaccttgaaggtcttc:3375
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            5.1.4_p5_4578
Compugen Ltd.
                                                                                                                                                                                                     residues
                                                                                                                                                                                                                                               of hits satisfying chosen parameters:
            GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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                                                        nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Minimum DB : Maximum DB :

Database

Total number

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Title: Perfect :

Sequence:

OM nucleic

Run on:

Scoring table:

Tel: +55-11-2704922 Fax: +55-11-2707001

UI-E-CQ1-RPCI11-58 PM1-CT026 UI-H-BIl-

AW206492 UBE143292 NBM702190 UA0202422 FAW855319 E

BF849816 AW206492 BE143292 BM702190 AQ202422 AW855319

12 10 17 17

535 406 282 723 496 567

305 296 128 113 69 69

MR0-HT016

BF849816 PM4-EN006

Description

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DB

Length

Score

Result ٠ يو

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/note="Organ: lung_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A min1:library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-EN0068-151100-004-b06&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 534.
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NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW206492
UI-H-BII-aez-c-01-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2721001 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2899 CCCACTTTCTGTACCTGCTGTGCCTTGTTGAGGCTATGTCATCTGCCACCTTTCCCTTGA 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2959 GGATAAACAAGGGGTCCTGAAGACTTAAATTTAGCGGCCTGACGTTCCTTTGCACACAAT 3018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 CAATGCTCGCCAGAATGTTGTTGACACAGTAATGCCCAGCAGAGGCCTTTACTAGAGCAT 356
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                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="EN0068"
                                                                                                                                                                                                                                                                           /dev_stage="Adult"
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Unpublished (1997)
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Matches 305; Conservative
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strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2676 TCCCAGCAACTACAGAGAAGGCCTGGGCACTGAAATGGTGCCTACCTTCTGGAATGTCTG 2735
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100.0%; Pred. No. 1.1e-136;
1ive 0; Mismatches 0;
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                                                                                                                   1. 406 /organism="Homo sapiens"
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                                                                                                                                                /db_xref="taxon:9606"
                                                                                                       Location/Qualifiers
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="HT0161"
/dcv_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0161-221
099-002-c08&t3=1999-10-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 282.
Location/Qualifiers
                                                                                                                                                        EST 21-JUN-2000
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                                                                                                                                          bE143292
MRO-HT0161-221099-002-C08 HT0161 Homo sapiens CDNA, mRNA sequence.
BE143292
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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2856 CCACAAACGATGTTGAAAAGTTTTGATGTGTAAGTAAATACCCACTTTCTGTA 2911
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Similarity 100.0%; Pred. No. 1.7e-52;
28; Conservative 0; Mismatches 0;
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1. 723
/organism="Homo sapiens"
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BM702190 723 bp mRNA linear EST 28-FEB-2002 UI-E-CQ1-aey-m-08-0-UI.rl UI-E-CQ1 Homo sapiens cDNA clone UI-E-CQ1-aey-m-08-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 723) Bonaldo, M.E., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2615 GGATTCTTGAGACGCCCCTGAGGCACATGGCTCCCGTGCAGGAGGGCAGCAGCGTACCC 2674
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The following repetitive elements were found in this cDNA sequence: 353-608, >LinE2 Seq primer: M13 Reverse.
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Program for Rat Gene Discovery and Mapping
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1larity 100.0%; Pred. No. 6.6e-45;
Conservative 0; Mismatches 0;
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Matches 113; Conserv
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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 5 AQ202422

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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201 bp mRNA linear EST 19-MAY-2000 RC1-CT0286-050400-018-e03 CT0286 Homo sapiens CDNA, mRNA sequence. AW856235 AW856235.1 GI:7951928 EST.
                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=PM1-CT0268-221 099-002-e08&t3=1999-10-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence start: 23
Location/Qualifiers
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 567)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Scuzu, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A mini-library was made by cioning products derived ORESTES PCR (U.S. Letters Patent application No. 196 - Ludwig Institute for Cancer Research) profiles the pUC 18 vector. Reverse transcription of tissue and cDNA amplification were performed under low
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

[ Dasses 1 to 201)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Botdin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0268"
/dow_stage="Adult"
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived
                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig-Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             969 CACCAACGGCCTCTTCAGCACCCTCAGCAGCTCGGCCATCTGCTCCAGCGCCACGCCAG 1027
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hes 0;
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                                                 AUTHORS
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mRNA sequence.
                                                                                                                                               AQ202422 496 bp DNA linear GSS 20-APR-1999
RPCI11-58C10.TK RPCI-11 Homo sapiens genomic clone RPCI-11-58C10,
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                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Unpublished (1998)
Other_GSS: RPCIII-58C10.TJ
Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html class: BAC ends.
                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
a 103 c 128 g 133 t 3 others
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PMI-CT0268-221099-002-e08 CT0268 Homo sapiens CDNA,
AW855319
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are derived from the human BAC library
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7e-23;
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/db_xref="GDB:7521945"
/db_xref="taxon:9606"
/clone="RRCI-11-58C10"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                         DNA sequence.
AQ202422
AQ202422.1 GI:3609893
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Konno, H., Okazaki, Y.,
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BB613951
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                                                                                                                                                               Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-CT0286-050
400-018-e03&t3=2000-04-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 200
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: colon; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patcht application No. 196, 716 - Ludwig Institute for Cancer Research) profiles
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URL:http://genome.gsc.riken.go.jp/
Carnincl,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                   Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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hes 0; Indels
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100.0%; Pred. No. 6.2e-
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/db_xref="taxon:9606"
/clone_lib="CT0286"
/dev_stage="Adult"
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Contact: Yoshihide Hayashizaki
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BB612001.1 GI:16453080
                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawal, J., Shibata, K. and
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modified pBluescript KS(+) after bulk excision from Lambda
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        Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Hatahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura Hayashizaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched, 15 days embryo
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Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
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/strain="C57BL/6J"
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/clone="4022422118"
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ORGANISM

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                                                                               Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.; Sano, H., Sasaki, D., Shibara, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., RKEN, Mouse ESTS, (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)

10 (11), 175-1771 (2000)

Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) (2005). Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penes: Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(6SC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4832416c0:10
/clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="head"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
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1. .638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
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FEATURES

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Arakawa, T., Carnioci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishli, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, M., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shraki, T., Sogabe, Y., Guzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M., and Hayashizaki, Y.
ENIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 26-OCT-2001
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URL:http://genome-gsc.riken.go.jp,
Carnindi.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carnindi.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
agai.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
K.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB617396 664 bp mRNA linear EST 26-OCT-2001
BB617396 RIKEN full-length enriched, 11 days pregnant adult female
ovary and uterus Mus musculus CDNA clone 5031412M06, mRNA sequence.
BB617396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 664)
3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." 192 c 182 g 133 t
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Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                           Length 638;
                                                                                                                                                                                                                                           DB 10; L
0.00081;
                                                                                                                                                                                                                                       0.9%; Score 31; DB 100.0%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                    614 GITCCACTCCTCATCTGGAATTCCCCTTGGA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .664
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BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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MEDLINE
COMMENT
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BG991167
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                                              FEATURES
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                                                                                                                                                           Bos taurus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Crantiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases I to 501)
Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,
Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett
G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G.,
Reele, J. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 25-APR-2001
                                    /clone="5031412M06"
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                          /note="Site_1: Sall; Site_2: BamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 10; Length 664;
Pred. No. 0.00081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF601265 501 bp mRNA linear 266197 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                         /tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 0.9%; Score 31; DB Local Similarity 100.0%; Pred. No. 0.0 nes 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Mus musculus"
                              'db xref-"taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAACAGCTATGACCAT
           strain="C57BL/6J
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BF601265.1 GI:11698487
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Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORIGIN
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BF601265
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MEDLINE
COMMENT
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukarwyota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 148)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Ragai, M.A., de Silva, W. Jr., Raguskiwa, A., Baia, G.S., Simpson, D.H., Brunstein, A., Geoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Scuza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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MR2-HT1189-270101-003-h07 HT1189 Homo sapiens CDNA, mRNA sequence.
BG991167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-HT1189-270101-003-h07&t3=2001-01-27&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                /tissue_type="pooled"
//lab_host="phil0"
//note="vector: pcWv SPORT6; Site_1: Not1; Site_2: Sal1;
//note="vector: pcWv SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.9%; Score 30; DB 12; Length 501; Best Local Similarity 100.0%; Pred. No. 0.0025; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2547 TGGCTGGGAGGCCCCCCACTGCGAGACCG 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 TGGCTGGGAGGCCCCCACTGCGAACCG 53
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High quality sequence stop: 147
Location/Qualifiers
Plate: 40 row: J column: 10
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG991167.1 GI:14395237
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                                                                                    1. .501
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BASE COUNT ORIGIN

Matches

ò g RESULT 13 AA910328/c

DEFINITION

LOCUS

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
    Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.lnl.gov/bbrp/image/image/image.html
Insert Length: 589 Std Error: 0.00
Seq primer: -400P from Gibboo.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Crgan: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCK-amplified cDNAs from a pool of 5,000 clones made from the same library [cloneIDs 1322376-1323911, 1456007-1456775, and Ibrary 150052-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
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  p mRNA linear EST 17-DEC-1999 sapiens cDNA clone IMAGE:2316914 3'
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumania!: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 474)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 445)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                   wc32q02.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:Similar to TR:060494 060494 INTRINSIC FACTOR-B12 RECEPTOR PRECURSOR.;, mRNA sequence.
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        445 bp
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 395)

1. (Dases 1 to 395)

NOTI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Timor Gene Index

Tumor Gene Index

Tumor Gene Index

Tumor Gene Index

Trissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Parayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40mil ffers

Location/Qualifiers
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                  395 bp mRNA linear EST 13-APR-1998 similar to TR:Q23242 Q23242 ZC116.3; mRNA sequence.
AA910328 G::3049618 EST.
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 43~c~47~g~29~t~
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                                                                                                                                                             0.9%; Score 29; DB 13; Length 148; 100.0%; Pred. No. 0.0064; Live 0; Mismatches 0; Indels
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RESULT 14 AI744019/c

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BASE COUNT ORIGIN

Sequencing Center information can be

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.ntml
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/lab_host="DH10B"
                           Unpublished (1997)
Other_ESTs: qz39a03.x1
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:2029228"
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Search completed: May Job time : 3012 secs

411 CTGCCAGAATGGAGCACATGTGTT 435

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(without alignments) 17085.053 Million cell updates/sec 1 gacagtgttcgcggctgcac......tgtccaccttgaaggtcttc 3375 4, 2003, 22:50:07; Search time 5749 Seconds 4109280 2054640 segs, 14551402878 residues Potal number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_htgo_other:* em_htg_inv:* em_htg_other:* em_htgo_hum:* htgo_mus:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 em_htg_hum: * em_htg_mam:* em_htg_vrt:* em_htg_rod:* em_htg_pln:* US-09-930-020A-1 em_htq_mus: gb_ro:* gb_sts:* gb_sy:* em_ba:* em_fun:* em_hum: em_or:* em_ov:* em_ph:* em_sts: gb_ba:* gb_htg:* gb_pat: * gb_ph: * gb_pl: * gb_un:* gb_vi:* em_un:* em_v1:* em_in:* gb_om:* em_mu: em_pat em_om: em_ro: GenEmbl:* Мау Title: Perfect score: Scoring table: OM nucleic Sequence: Searched: Database Run on:

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AC095899 Mus muscu AC181619 Sequence AC119647 Rattus no M14792 Chicken car M55683 Human carti AB04043 Homo sapi AC112730 Rattus no U35035 Mus musculu AC06262 Mus musculu U32107 Mus musculu U32107 Mus musculu AC06140 Mus muscul AC06140 Mus muscul AC06141 Mus muscul AC06141 Rattus no AC096154 Rattus no AC127063 Rattus no AC127063 Rattus no M55679 Human carti Human DNA Homo sapi Mus muscu Homo sapi Homo sapi Mus muscu AC105383 Homo sapi AC119647 Rattus no AC125150 Mus muscu Homo sapi Homo sapi Homo sapi Homo sapi Sequence Homo sapi U69263 Homo sapien AF314058 Homo sapi X12350 Chicken car AX079876 Sequence Sequence AX399978 Sequence AX399977 Sequence AR085071 Sequence AL021578 Human DNA AX079878 Sequence Homo sap AX464160 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AL137857 BC010444 BC010444 BC010444 BC010444 BC010444 BC010444 BC010444 BC010444 BC010444 BC01044 BC01 AK027775 1 BC016394 F AX329755 SUMMARIES AX281619 AC119647 CHKCMP HUMCMPMR AB040943 AC112730 AC078821 AC097136 AC096154 AC127063 HUMCMP5 HSM802406 AL161942 AC099899 AL137857 BC010444 AX079878 AX464160 AX399977 AR085071 AX079876 21.1 123110 12.1 152895 12.1 154748 .5 1959 .4 190669 Length 4151 152895 3550 202006 194143 147620 189656 19281 15204 Query Score 712.6 408.6 408.6 317.8 309.8 123.4 776.6 Result õ O

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                                                                Smith.D.R.
Direct Submission
Submitted (31-0CT-1998) Genome Therapeutics Corporation, 100 is Street, Waltham, MA 02154, USA
On Oct 31, 1998 this sequence version replaced gi:3808081.
Location/Qualifiers
1. 123110
1. 123110
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                                                                                                                                                                                                                          Length 123110;
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Pred. No. 4.2e-141;
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                                                                                                                                          /organisme"Homo sapiens"/db_xref="taxon:9606"
/chromosome="10"
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Submitted (05-AUG-1998) Genome
Street, Waltham, MA 02154, USA
3 (bases 1 to 123110)
          to 123110)
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Best Local Similarity 98.4%;
Matches 751; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20340380.
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contig of 1135 bp in 1
gap of unknown length
contig of 1613 bp in 1
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                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
                                        Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown l
contig of 1121 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown l
of 1626 b
unknown l
of 1255 b
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of 1261 k
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of 1452 b
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                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently tonsists of 8 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 154748;
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gap of unknown length
contig of 2738 bp in length
contig of 2738 bp in length
contig of 31778 bp in length
gap of unknown length
contig of 4530 bp in length
gap of unknown length
contig of 10988 bp in length
contig of unknown length
gap of unknown length
gap of unknown length
                                                                                                                                           Insert size: 164000; agarose-fp
Insert size: 154048; sum-of-contigs
Quality coverage: 8 91 in 020 bases; sum-of-contigs
Quality coverage: 8.71 in 020 bases; sum-of-contigs
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gap of unknown length
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 151541 bases at least Q40
Consensus quality: 151970 bases at least Q20
Consensus quality: 152209 bases at least Q20
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/note="assembly_name:Contig12"
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/note="assembly_name:Contig13"
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/note="assembly_name:Contigl1
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/db_xref="taxon:10090"
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Parkway, St. Louis, MO 63108, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                       86237 CTGCTACTCCTGGGCATGGGAAATGAGCTCATGCGGGCAGAGCTGGAGGATCACGGGT 86296
85877 GGCACCACTCCGGAGGGTTTCCGTCAGGCCAAGGCCTTTGTGAAGCGCTTTGTGCAGGCC 85936
                                                                                                                                                                                                                                             ATTCCCTTCCGTGGTGGCCCCCACCCTGACGGCCAGTGCCTTGCGGCAGGCGCAGAGCGT 1623
                                                                                                                                                                                                                                                                                                                                         GGCTTCGGGAGCGCCACCAGGACAGGCCAGGACCGGCCACGTAGAGTGGTGGTTTTGCTC 1683
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Mus musculus chromosome UNK clone RP24-354K9, WORKING DRAFT
                                               1444 GTGCTGAGCGAGGACTCTCGGGCCCGAGTGGGTGTGGCCCACATACAGCAGGGAGCTGCTG
                                                                                                                                              GTGGCGGTGCCTGTGGGGGAGTACCAGGATGTGCCTGACCTGGTCTGGAGCCTCGATGGC
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Center code: WUGSC
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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McPherson, J.D. and Waterston, R.H.
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Sequencing vector: plasmid; 100%
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Submitted (22-JUN-2001) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
4 (bases 1 to 160420)
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                                   Db 108885 CTACTCCTCGTGGGCGTGGGCAGTGAGATCCTGCAGGCGGAGCTGGTGAAGATCACCGGT 108944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 108945 AGCCCGAAGCATGTGATGGTCCACACACACACTCTCAGCACCTGTTCAGCCCAAATCCCAGAG 109004
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Smith, D.R.
Genome Therapeutics Corporation Sequencing Center: Human Genome
                                                                                                                                 Db 108645 GTGGCGGTGCCCGTCGGGGAGTACCAGCATGTGCCGGACCTGATCAGGAGCCTTGACAGC 108704
Db 108525 GGCACCACATTGGGGGGCTTCCGGAGGGCCAAGGCCTTTGTCAAGCGCTTTGTGCAGGCC 108584
                                                                                                                                                                                                          DD 108705 ATTCCCTTCAGCGGTGGCCCGACCCTAACCGGGAGTGCCTTGCTCCAGGTGGCAGCAGCAC 108764
                                                                                                                                                                                                                                                                                 DD 108765 GGCTTTGGGAGTGCCAGCAGGACTGGTCAGGACAGGCCACGCAGAGTAGTAGTTCTGCTC 108824

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    1684
    ACTGAGTCACACTCCGAGGATGAGGTTGCGGGCCCAGCGCGTCACGCAAGGGCGCGAAGGG
    1743

    Db
    108825
    ACTGAATCACGCTCCCAGGATGAGGTCTTGGGCCAGCAGCTCACGCAAGGCCTCGGGAG
    108884

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                                                                                                                                                                                        1564 ATTCCCTTCCGTGGTGGCCCCACCTGACGGCAGTGCCTTGCGGCAGGCGGCAGAGCGT 1623
                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTCCTGCTGGGTGTAGGCAGTGAGGCCGTGCGGGCAGAGCTGGAGGAGTCACAGGC 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCCAAAGCATGTGATGGTCTACTCGGATCCTCAGGATCTGTTCAACCAAATCCCTGAG 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (25-JAN-2000) Genome Therapeutics Corporation, 100
Street, Waltham, MA 02453, USA
3 (bases I to 160420)
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                                                                                                              GTGGCGGTGCCTGTGGGGGGGTACCAGGATGTGCCTGACCTGGTCTGGAGCCTCGATGGC
                                                                                                                                                                                                                                                               GCCTTCGGGAGCGCCACCAGGACAGGCCAGGACCGGCCACGTAGAGTGGTGTTTTGCTC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-411P18"
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Homo sapiens
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 136357)

8 Burton, J.

8 Burton, J.
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Homo sapiens chromosome 20 clone RPII-83B5, *** SEQUENCING IN
PROCRESS ***, 33 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CTGGCGGTAGTTCCTCCGACCTCAGCCGGGTCGGGTCGTGCCGCCCTCTCCCAGGAGAA 181
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                                                                                                                                                                                           Length 160420;
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                                                                                                                                                                                           Query Match 9.4%; Score 317.8; DB 9; Best Local Similarity 95.1%; Pred. No. 3.8e-57; Matches 328; Conservative 0; Mismatches 17;
/clone_lib="RPCI-11"
48686 a 32379 c 32258 g 47097
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HTG: HTGS_PHASE1; HTGS_CANCELLED
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/chromosome="20" /clone="RP1-83B5" /clone=lib="RPCI-11.1" 1. 5425 /note="assembly_fragment:01370 fragment_chain:1 clone_end:SP6 vector_aide:left" 5526. 9483 /note="assembly_fragment:01120 fragment_chain:1" 5548. 14280 /note="assembly_fragment:00095 fragment_chain:1" 9584. 14280 /note="assembly_fragment:00095 fragment_chain:1" 14381. 17312	fragment_chain:1" 1413. 22848 /note="assembly_fragment:00025 fragment_chain:2" 22949. 26090 /note="assembly_fragment:00387 fragment_chain:2" 26191. 28215 /note="assembly_fragment:00262 fragment_chain:3" 28316. 33862 /note="assembly_fragment:00134 fragment_chain:3" 33963. 44145 fragment_chain:3" 33963. 44146	Itagament_Canain:4" 4124653165 /note="assembly_fragment:00989 fragment_chain:4" 5326657410. /note="assembly_fragment:00876 fragment_chain:5" 5751360170 /note="assembly_fragment:00248 fragment_chain:5" 6027165985 /note="assembly_fragment:01554 fragment_chain:6" 608665984 /note="assembly_fragment:0156 fragment_chain:6" 6019571736 /note="assembly_fragment:00470 fragment_chain:6" 619571736 /note="assembly_fragment:01566 fragment_chain:7" 7183774955 /note="assembly_fragment:01566 fragment_chain:7" fragment_chain:7" fragment_chain:7" fragment_chain:7"	1.09umul. 7.7325 /note="assembly_fragment:00036" /7426. 80709 /note="assembly_fragment:00390" 80810. 82943 /note="assembly_fragment:00409" 83044. 85218 /note="assembly_fragment:00437" 8519. 98961 /note="assembly_fragment:00764" 8962. 9282. 98861 /note="assembly_fragment:00764" 8962. 92925. 98822 /note="assembly_fragment:00808" 95923. 98130 /note="assembly_fragment:00808" 96931. 100594 /note="assembly_fragment:008186" 100695. 109043
misc_feature misc_feature misc_feature misc_feature	misc_feature misc_feature misc_feature misc_feature	misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature	misc_feature
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, but sit if year in the control of	28215: contig calls: contig calls: gap of 3362: gap of 44145: contig calls: cal		100641: gap of 100 bp 109043: contig of 8349 bp in 109143: gap of 100 bp 112146: gap of 100 bp 112246: gap of 100 bp 117246: gap of 100 bp 11783: gap of 100 bp 1121861: contig of 4578 bp in 124258: contig of 4578 bp in 124258: contig of 2297 bp in 124258: gap of 100 bp 127136: gap of 100 bp 137357: contig of 6221 bp in 13757: gap of 100 bp in 13357: contig of 6221 bp in 13357: contig of 2900 bp in cation/oualifiers
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14421: gap of
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus clone RP23-12A20, LOW-PASS SEQUENCE SAMPLING.
AC099899
                                                                                                                                                                                                                                                                                                                                                          Length 136357;
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-12A20
                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                            Score 309.8; DB 2;
Pred. No. 1.9e-55;
0; Mismatches 22;
                                                       'note="assembly_fragment:01604"
27571 c 27577 g 39953 t 3
      /note="assembly_fragment:01007"
112247. .117183
                                                                                                                                                                                                                               /note="assembly_fragment:01498"
133458. .136357
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Best Local Similarity 93.6%;
Matches 323; Conservative C
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Meneus, L., Mihova, T., Macralan, M., Marphy, T., Maylor, J., Muyby, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollara, J., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange-Thomann, N. Stojanovic, N. Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Valla, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J
                                                                                                                                                                                                                                                        Submitted (22-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 82 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is complete, y arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          690 789: gap of 100 bp
790 1505: contig of 716 bp in length
1506 1605: gap of 100 bp
1606 2298: contig of 693 bp in length
2299 2398: gap of 100 bp
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of 694 bp in length
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f 672 bp in length
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f 704 bp in length
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f 698 bp in length
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f 692 bp in length
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f 720 bp in length
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f 713 bp
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10289: contig of 686 bp
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Center clone name: 12_A_20
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12009 12714: conti
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13516: con
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7088: c
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6268:
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23 37701: gap of 100 bp 11 length 10 8509: gap of 100 bp 11 39210: contig of 708 bp in length 11 39210: contig of 708 bp in length 11 39210: gap of 100 bp 11 40022: contig of 712 bp in length 23 40122: gap of 100 bp 23 40834: contig of 712 bp in length 23 40834: contig of 712 bp in length 10 bp 100 bp 
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36781: contig of 683 bp in length
881: gap of 100 bp
37601: contig of 720 bp in length
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22381: contig of 682 bp in
22481: gap of 100 bp
23192: contig of 711 bp in
3 23292: gap of 100 bp
23998: contig of 706 bp in
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                              100 bp [ 705 bp ] [ 705 bp ] [ 701 bp ] [ 700 bp ] [ 709 bp ] [ 709 bp ] [ 696 bp ] [ 703 bp ] [ 704 bp ] [ 70
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44060: contig of 699 bp
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5 17543: contig of 70
4 17643: gap of 10
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                          217: gap of 10
15922: contig of 7
022: gap of 10
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33578: contig of 78: gap of 1
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16734: contig of
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31165: contig of 65: gap of 1
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ACU99899 65824 bp DNA linear HTG 22-NOV-2001
MUS musculus clone RP23-12A20, LOW-PASS SEQUENCE SAMPLING.
AC099899
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-12A20
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0; Mismatches 41
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51298: contig of 695 bp
51398: gap of 100 bp
52111: contig of 713 bp
44160: gap of 100 bp
44844: contig of 684 bp
44944: gap of 100 bp
45650: contig of 706 bp
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490: gap of 100 bp 35199: contig of 709 bp in len
70: gap of 100 bp in len
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-^4 bp 4
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116: gap of 100 bp 17125: contig of 709 bp 1.
225: gap of 100 bp 1.
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      Hagos, B., Haeford, A., Karatas, A., Kells, C., Lakone, F., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakone, K., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakone, K., Liu, G., MacCean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Morman, C.H., O'Connor, K., Marphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Ye, W.J., Young, G., Direct, Submission
                                                                                                                                                                                                                                         Submitted (122-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
Graham, L., Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
of 692 bp in length
100 bp
of 699 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
of 713 bp in length
100 bp
of 704 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 689: contig of 689 bp in length 1690 789: gap of 100 bp 790 1505: contig of 716 bp in length 1506 1605: gap of 100 bp 1606 22298: contig of 693 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11201: gap of 100 by
11908: contig of 707 bp in length
12008: gap of 100 bp
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f 694 bp in length
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if 672 bp in length
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f 713 bp in length
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f 720 bp in length
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698 bp in length
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686 bp in length
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8805: gap of
9503: contig of
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                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 12_A_20
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11101: con†
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JOURNAL
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Gaps

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E I (bases 1 to 152895)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blangec, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Brimage, K., Blankenburg, K., Bonnin, D., Buvek, J., Bowie, S., Brieva, M., Brown, E., Brown, M. Bryant, N.P., Buvek, C., Burcall, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Osovy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACLIBER HTG 18-JUL-2002 Rattus norvegicus clone CH230-137H14, *** SEQUENCING IN PROGRESS ***, 54 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                             1188 TGGTCTTCCTCATTGACGGATCCAAGAGTGTGAGGCCAGAGAACCTTGAGCTGGTGAAGA 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 AGTICATCAGICAGAICGIGGAIACGCIGGACGIGICAGACAAGCIGGCCCAGGIGGGGC 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1368 AGGACATCAAGGCGGCTGTGCGGAATATGTCCTACATGGAGAAGGGCACAATGACGGGG 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1488 CCCAGAAGGTGGGGATTGTCTTCACTGATGGCGGGGCCAGGACTACATTAATGATGCTG 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1548 CCAAGAAGGCCAAAGACCTCGGCTTTAAGATGTTTGCTGTGGGTGTGGGCAATGCCGTGG 1607
                                                                                                                                                                                                                                                                                 422 AAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATGTGGTGCTCGGCTGCAGTGGACA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCCCAGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGCACTGCCAT 835
                                                                                                                                                                                                                                                                                                                                                                    482 TCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGGAGCTTTGAAAGGTCCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 ACTITICCCATCACAGTCTGTGACGGTCTGGACATCAGCCCCGAGAGGGTCAGAGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 CATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              722 TTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATGCT----TCTG
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                            82 others
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                                                                                                               Score 97.8; DB 6; Pred. No. 2.8e-10; 0; Mismatches 253;
/note="Incyte ID No: 980611.1"
1089 c 1163 g 928 t
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Mammalia; Eutheria;
                                                                                                                                                                                  Matches, 265; Conservative
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Rattus norvegicus
                                                                                                                        Query Match
Best Local Similarity
                            889 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ***, 54 u
AC119647
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AC119647/c
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                               BASE COUNT
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KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2503 AGCTGCGTCCTGCAGAATGGGAGCTACCGCTGCAAGTGTCGGGATGGCTGGGAGGGCCCC 2562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shiffman, D., Somogyi, R., Lawn, R., Seilhamer, J.J., Porter, G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 65824;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52111: contig of 713 bp in length

2211: gap of 100 bp

52892: contig of 681 bp in length

592: gap of 100 bp

53712: contig of 720 bp in length

1812: gap of 100 bp

54517: contig of 705 bp in length
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55326: contig of 709 bp in length
55426: gap of 100 bp
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Genes expressed in foam cell differentiation
Patent: WO 0177389-A 28 18-OCT-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111.8; DB 2;
Pred. No. 2.6e-13;
0; Mismatches 22;
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                                                                                                                                               44160: gap of 100 bp
44844: contig of 684 bp
44944: gap of 100 bp
45650: contig of 706 bp
                      63: gap of 100 bp
43261: contig of 698 bp
161: gap of 100 bp
44060: contig of 699 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
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   contig of
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24: gap of
54517.
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ilarity 85.0%;
Conservative
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DEFINITION ACCESSION

RESULT 8 AX281619

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REFERENCE AUTHORS

VERSION KEYWORDS

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Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hardgson, A., Hogdson, M., Hodgson, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kavar, C., Katly, S., Khan, U., King, L., Korvah, J., Kovar, C., Katovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Maheshwari, M., Mapue, P., Martin, R., Man, J., Martin, S., Martin, P., Martin, R., Marin, J., Martin, S., Martin, R., Marin, M., Morgan, M., Morser, M., Mapue, E., Mawhiney, E., McLeod, M. P., Martindale, A., Martin, S., Martin, R., Peters, L., Peters, L., Pickens, R., Prims, E., Payton, B., Perez, L., Peters, L., Pickens, R., Prims, E., Shoshtari, N., Sisson, I., Rolfe, M., Rojas, A., Taylor, P., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, A., Svatek, A., Taylor, P., Tamerisa, A., Tamerisa, R., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, P., Taylor, P., Villalon, D., Vinson, R., Wang, K., Walliamson, A., Walliams, G., Walliamson, A., Waler, R., Washington, C., Walliams, G., Walliamson, A., Mleczyk, R., Wooden, S., Warley, R., Wuy, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Well, R., Handley, R., Man, Y., Wuy, Y., Wuy, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Well, R., Handley, R., Man, Y.F., Shomley, R., Wooden, S., Warley, R., Walliams, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submission Submitted (18-JUL-2002) Human Genome Sequencing Center, Department Submitted (18-JUL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced g1:20340380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (30-APR-2002) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 152895)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 9174 bases at least Q40
Consensus quality: 95583 bases at least Q20
Consensus quality: 103878 bases at least Q20
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1141: gap of unknown length
2262: contig of 1121 bp in length
2362: gap of unknown length
3497: contig of 1135 bp in length
3597: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: CH230-137H14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GVPZ
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COMMENT

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/translation-"VGVINYASAVKNEFSLKTHQTKAELLQAVQRIEPLSTGTWTGLA
IQPAISRAFSOTDGARLASPNINKVALTVYTDGRORDGVOVDSARARQAGIEIFALGVG
RVDMFTLRQIASEPLDHUDVBVESSYVIEKTHRFQBAFCVVSDLCATGDHDGEQICI
STPGSYKCACKEGFTLNNDGKTCSACSGGSGSALDLVFLIDGSKSVRPENFELVKKFI
SQLVESLEVSEKQAQVGLVQYSSSYVRDEPLQGFKKKRDIARAVKKMAYBKGTWTGQ
ALKXIVDSSFSIANGARPGVPKVGIVFTDGRSQDYITDAAKKANDLGFRANFACGVURAG
VEDELREIASEPVAEHYFYTADFRIISNIGKKLQMKICVEEDPCECKSIVKFQTKVEE
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M55683 J GI:180651
cartilage matrix protein.
Human, cDNA to mRNA.
                                                                                                                                                                                                                                                                                 Length 1364;
                                                                                                                                                                                                                                                                              Score 95.6; DB 5; Length 1
Pred. No. 8.7e-10;
0; Mismatches 224; Indels
                                              /note="cartilage matrix protein"
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359 a 304 c 362 g 279
1299 bp upstream of EcoRI site.
                                                                            /protein_id="AAA48695.1"
/db_xref="GI:211546"
                /product-"CMP mRNA"
                                                               /codon_start=]
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Best Local Similarity 51.7%;
Matches 246; Conservative (
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Chicken cartilage matrix protein mRNA, 3' end.

M14792

M14792

M14792

M14792

M14792.1 GI:211545

Scartilage matrix protein. matrix protein.

Chicken 14 day-old embryo sternum, cDNA to mRNA, clones pCMP[4,6].

ISM Gallus gallus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

S Argraves,W.S., Deak,F., Sparks,K.J., Kiss,I. and Goetinck,P.F.

Structural features of cartilage matrix protein deduced from cDNA

E Proc. Natl. Acad. Sci. U.S.A. 84 (2), 464-468 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-MAR-1987.
The cartilage matrix protein mRNA is first detectable in day 5 limb
buds. Its expression is cartilage-specific and developmentally
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/organism="Gallus gallus"
/db_xref="taxon:9031"
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Pred. No.
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Best Local Similarity 79.2%;
Matches 114; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

RESULT 10 CHKCMP

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FEATURES

REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED

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QTEAPGNATSAMLGPLSSSTTYTVRVTCLYPGGGSSTLTGRVTTKKAPSPSQLSMTEL
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Mammalia; Eutheria; Primates;
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Location/Qualifiers
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<1. .3425
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/gene="KIAA1510"
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/product="cartilage matrix protein"
/protein id="AAA63904.1"
/protein id="AAA63904.1"
/protein id="1806504.1"
/db_xref="GDB:000-127-280"
/translation="PQDSVQDVSARARASGVELFAIGVGSVDKATLRQIASEPQDEHV
PYESSYSTERREPERFVYSDLCATGOHDGZOVCISSESSYRCARGFTLNSD
GKTCNVCSGGGGGSARTLLVFLIDGSKSVREPRILELVKKFISQIVDTLDVSDKLAQVGL
VQYSSSYROEFPLGRFHTKKDIKAAVRNMSYMEKGTMTGAALKYLIDNSFTVSSGARP
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YTADFKTINQIGKKLQKKICVEEDPCACESLVKFQAKVEGLLQALTRKLEAVSKRLAÌ
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Pred. No. 8.3e-10;
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                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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              Location/Qualifiers
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/gene="CRTM"
/note="G00-127-280"
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/gene="CRTM"
/note="G00-127-280"
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/gene="CRTM"
/note="G00-127-280"
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/gene="CRTM"
/note="G00-127-280"
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/gene="CRTM"
/note="G00-127-280"
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/gene="CRTM"
/note="G00-127-280"
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/clone="pHCMP2"
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Submitted (04-APR-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL.http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"PSQDPRTPGGSEWRETGPQFRCLPPVPADMVFLVDGSWSIGHSH
FQQVKDFLASVIAPPEIGPDKVQVGLTQYSGDAQTEWDLNSLSTKEQVLAAVRRLRYK
GGNTFTGLALTHVLGQNLQPAAGLRPEAAKVVILVTDGKSQDDVHTAARVLKDLGVNV
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PAAGTELHNIASRTEYLJVSVPPIYEGGVGEGIRGLVTTAPLPPRALTJAAVTPRTVH
PROPSAGATHYLVRCSPAPRGEEEREVOVGRPVLLJGLEPGRDYEVSVOSLRGP
EGSBARGIRARPTLAAPRHIGFSDVSHDAARVFWEGAPRPVRLVRVTYVSSEGGHSG
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase,T., Kikuno,R., Ishlkawa,K., Hirosawa,M. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 7 (2), 143-150 (2000)
539 AGGACATCAAGGCGGCTGTGCGGAATATGTCCTACATGGAGAAGGGCACAATGA.CGGGG 598
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                                                                                                              836 CCAAGCAGCTGAAGGAAAGGGGTGTCACTGTGTTTTGCTGTGGGGGTCAGGTTTCCCAGGT
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Homo sapiens mRNA for KIAA1510 protein, partial cds.
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                                                                        722 ITGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATGCT
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/organism="Homo sapiens"
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NA linear HTG 10-JUL-2002
*** SEQUENCING IN PROGRESS ***,
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PGDAVQLAWVAAAPSGVLVYQITWTPLGEGKAHEISVPGNLGTAVLPGLGRHTEYDVT
                   ILAYYRDGARSDPVSLRYTPSTVSRSPPSNLALASETPDSLQVSWTPPLGRVLHYWLT
XAPASGLGPEKSVSVPGARSHVTLPDLQAATKYRVLVSAIYAAGRSEAVSATGQTACP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsovoks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carren, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, L., Chwidhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AGGTCAAGGACTTCCTGGCCAGTGTCATCGCACCCTTTGAAATCGGGCCGGATAAGGTCC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                         202 AAGTAGGCCTGACTCAGTACAGCGGGGATGCTCAGACTGAGTGGGACCTGAACTCCCTCA 261
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Pred. No. 3.6e-08;
0; Mismatches 222; Indels 6
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Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Ealls, T., Eacy, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hade, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, M., Mapus, P., Martin, R., Martindale, A., Martinez, E.,
Mahshwari, M., Mapus, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Mardor, M., Morris, S.,
Moser, M., Nall, D., Newtson, J., Newtson, N., Neugan, M., Neugar, M., Newtson, S.,
Cragunye, N., Oviedo, R., Pare, M., Ele, M., Ruiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sison, I.,
Sodergren, E., Sonaike, T., Sparks, A., Tamerisa, R., Tang, H.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, M., Thomas, S.,
Tansey, J., Taylor, C., Telfcod, B., Thomas, S.,
Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williamson, A., Willsen, R., Williamson, A., Waren, R., Washington, C., Wallington, C.,
Walliamson, A., Waren, R., Washington, C., Wallington, S.,
Wellse, S., March, R., Washington, C., Wallington, S.,
Wellse, S., March, S., Warren, R., Washington, C., Walling, S.,
Wellse, S., Warren, S., Warren, R., Washington, C., Walling, S.,
Wellse, S., Walling, S., Warren, R., Washington, S., Walling, S., Warren, C., Walling, S., Warren, S., War
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* (see http://www.hgsc.bom.tmc.edu/docs/Geabank_draft_data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 70 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 194143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 131293 bases at least Q30
Consensus quality: 142936 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Pred. No. 5e-08;
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KEYWORDS
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ATDLYFLIDGSKSYRPENFELVKRFINQIVDTLDVSDRLAQVGLVQYSSSTRQFFPLG
ATBLYKLDIKARVRNMSYMEKGTMTGAALKYLIDNSFTVSSGARPGAQKVGIVFTDGRS
QDYINDAARRAKDLGFKMFAYGVGRAVEEELREIASEPVADHYFYTADFKTINQIGKK
LQKOICVEEDPCACESILKFEAKVEGLLQALTRKLEAVSGRLAVLENRII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKVTSGPASALCSLLLLLLLLLQVPDSLSLYPOPRGHLCRTRPT
DLVFVVDSSRSVRPVEFEKVKVFLSQVIESLDVGPNATRVGLVNYASTVKPEFPLRAH
GSRASLLQAVRRIQPLSTGTWTGLALQFAITKALSDAEGGRARSPDISKVVIVVTDGR
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                                                                                                                                                                                                                                                                    Submitted (30-AUG-1995) Attila Aszodi, Agricultural Biotechnology Center, Institut for Animal Sciences, Szent-Gyorgyi Albert 4., Godollo H-2101, Hungary On Jan 23, 1996 this sequence version replaced gi:1144533.
                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                 Cloning, sequencing and expression analysis of mouse cartilage
                                                      1 (bases 1 to 1959)
Aszodi,A., Hauser,N., Studer,D., Paulsson,M., Hiripi,L. and
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/protein_id="ARB0651.1"
/db_xref="Gi:1163179"
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note="putative"
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Pred. No. 1.5e-07;
0; Mismatches 230; Indels
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                                                                                                                                                       Biochem. 236 (3), 970-977 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57 Black/6 X CBA"
/db_xref="taxon:10090"
/clone="mcCMP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="cartilage"
/dev_stage="adult"
/lab_host="Mus musculus"
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/gene="CMP"
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/gene="CMP"
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ilarity 49.2%;
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96270751
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                                                                                               Bosze, Z.
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Direct Submission.

Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 20, 2001 this sequence version replaced gi:15020991.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality)= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNEPP; Information or the WORNEPP database can be found at the sequence of the content of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL590429 190669 bp DNA linear ROD 17-NOV-2001 Mouse DNA sequence from clone RP23-462016 on chromosome 2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 190669)
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from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1188 TAATGACGCTGCCAGGAAGGCCAAGGACCTTAAGATGTTTGCGGTGGGCGTGGG 1247
948 CCAGGTGGGGCTGGTGCAGTACTCCAGCTCCATTCGCCAGGAGTTCCCACTCGGCCGCTT 1007
                                                                                                                                                                               1008 CCACTCCAAGAAGGACATTAAGGCGGGGGGGGGAACATGTCCTACATGGAGAAAGGCAC 1067
                                                                                                                                                                                                                                                                                                                                                                         CATGACTGGCGCCGCCTTGAAGTATCTCATAGATAATTCTTTCACTGTGTCCAGCGGGGC 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1128 AAGGCCTGGAGCCCAGAAGGTGGCCATCGTCTTCACCGATGGCCGGAGCCAGGACTACAT 1187
                                                                                            2271 AGCCGTTCCTGCCCAGAAGCTGAGGAACAATGGCATCTCTGTCTTTGGTCGTGGGCGTGGG
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                                                          Qy 1953 AGGCCCGAGAATTTTGCTCAGATGCAGAGCTTTGTGAGAAGCTGTGCCCTCCAGTTTGA 2012
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Pred. No. 5.3e-07;
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16-MAR-2001;
06-APR-2001;
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Oligonucleotide fo
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                   GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                           fotal number of hits satisfying chosen parameters:
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Listing first 45 summaries
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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynuclectides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical are differentially expressed in prostate polynuclectide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for useful for diagnosing or treating prostate cancer, as well as for infentifying modulators of prostate cancer or agents that inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer. The nucleic acid sequences are particularly useful
in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                    Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes
                                               ď,
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                                               Afar D,
                                                                                                                                                                                                                                                                  Claim 22; Page 376-377; 436pp; English.
                                                                                                                                                                                                                           tissue
                                             Wilson KE,
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  BIOTECHNOLOGY
                                                                                    WPI; 2002-471335/50
P-PSDB; ABG61891.
                                           Mack DH,
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                                                                  CAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGGAGACGGAA
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CGTGGCTTCGGGAGCGCCA 	CTCACTGAGTCACACTCCGI	GAGCTGCTCCTGCTGGGTG:	GGCAGCCCAAAGCATGTGA: 	GAGCTGCAGGGGAAGCTGT(CTCGTCTTCATGTTGGACA(AGCTTTGTGAGAAGCTGTGG 	CTGGTGGTGTATGGCAGCCJ 	GCTGCGATGCTGCGGGCCAT	ACCGCCTGCTGCACATCT/ 	GTCCCCAAAGCTGTGGTGGT 	GCCCAGAAGCTGAGGAACA/ 	AGTGAGGGTCTGCGGAGGC7 	GCCGACCTGCGGTACCACC/ 	CCAGTCAACCTCTGCAAACC 	GGGAGCTACCGCTGCAAGT(TGGAGCTCTTGCTCTGTATC	ATGGCTCCCGTGCAGGAGGC	GGCACTGAAATGGTGCCTAC
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INC.

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The invention relates to isolated polynucleotide (I) and

polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PGR) primers, oligomers, and for chromosome

and gene mapping, and in recombinant production of (II). The

confidentifying expressed genes. (I) is useful in gene therapy techniques

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC (II). (II) is useful for generating antibodies against it, detecting or

quantifating a polypeptide in tissue, as molecular weight markers and as

CC quantifating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical

magning of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in

C disorders involving aberrant protein expression of mutations

C disorders other types of data and products dependent on DNA and

CM and no acid sequences. Aas64197-Aas4564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC Note: The sequence data for this patent did not appear in the printed

CC Note: The sequence data for this patent did not appear in the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   printed
from WIPO
                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 17334; 103pp; English.
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1269 CAGGAAGTCCATGTAAGCAAAGAAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATG 1328 GGGAGCTTTGAAAGGTCCAAGCACTTTGCCATCACAGTCTGTGACGGTCTGGACATCAGC 1448 1688 579 639 669 759 819 879 400 CAGGAAGTCCATGTAAGCAAAGAAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATG 459 Gaps GGCAGAAATGCTTCTGTGCCCCCAGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGG TTGGATTCATTTTCAACCCAACAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAA GGAGGCGCACGGAGCGGAACTTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGA GGCAGAAATGCTTCTGTGCCCCCAGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGG CCCGAGAGGGTCAGAGTGGGAGCATTCCAGTTCCACTCCACTCCATCTGGAATTCCCC DB 23; Length 3485; 32; Indels 135; Score 2020.8; Pred. No. 0; .0; Mismatches 59.9%; 92.9%; Conservative Best Local Similarity Matches 2185; Conserv Query Match 640 200 520 1389 580 760 820 a ð ŏ qq ò g q δλ g δ g ò 셤 δý ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; andlogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
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                       CCTGACGTGACACAGGTCGGCCTGGTGTATGGCAGCCAGGTGCAGACTGCCTTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding murine skin cell secreted protein,
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dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocytes stem cells and transit amplifying calls. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAZG1606-Z61832 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences derived from several mouse, rat or human skin cell types. Sequences derived from several mouse, rat or human skin cell types. Sequences derived from several mouse, sequences AAZG1606-Z61780, AAZG1802-Z61813 and AAZG1827-Z61829 encode proteins with one or more putative
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The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
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 AGGCAGCCCAAAGCATGTGATGGTCTACTCGGATCCTCAGGATCTGTTCAACCAAATCCC
              CGGTAGCCCGAAGCATGTGATGGTCCACACACACACCCTCAGGACCTGT--CAGCCAAATCC
                                                                    Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnetary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; anglogenesis inhibition; inflammation; neurological disease; ss.
                                                        TGAGCTGCAGGGGAAGCTGTGCAGCCGGCAGCGCCAGGGTGCCGGACACAAGCCCTGGA
                                                                                                                                                                       GAGCTTTGTGAGAAGCTGTGCCCTCCAGTTTGAGGTGAACCCTGACGTGACACAGGTCGG
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33.1%; Score 1117.2; DB 22; Length 1837; 79.8%; Pred. No. 3.9e-267;

Query Match Best Local Similarity

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Human; rat; mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vulnerary; immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
                                                    CAGGCACCACTTGGGGGGCTTCCGGAGGGCCAAGGCCTTTGTCAAGCGCTTTGTGCAGG
                                           CCGTGCTGAGCGAGGACTCTCGGGCCCCGAGTGGGTGTGGCCACATACAGCAGGGAGCTGC
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        CGGGCACCACTCTGGACGGCTTCCTGCGGCCAAAGTCTTCGTGAAGCGGTTTGTGCGGG
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Kumble KD;
                                                                                 New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for modulating immune responses
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                                             Strachan
                            (GENE-) GENESIS RES
                                                               WPI; 2002-122020/16
24-MAY-2000;
25-JUL-2000;
                                             Watson JD,
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The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.

Sequence 1837 BP; 370 A; 541 C; 557 G; 369 T; 0 other;

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 DB 24; Length 1837;
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                       343; Indels
Score 1117.2; DB 24
Pred. No. 3.9e-267;
0; Mismatches 343;
 33.1%;
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2482 AGCCCGTGCATGAATGAGGGCAGCTGCGTCCTGCAGAATGGGAGCTACCGCTGCAAGTGT 2541
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
1774 GAGCTTCATCAGGAAATGCACCCTCCGGTTTGATGTGAATCCTGATGTGACACAAGTTGG 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.1%; Score 340; DB 23; Length 406; 90.7%; Pred. No. 2.1e-74; 1ve 0; Mismatches 0; Indels 4(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 406 BP; 80 A; 112 C; 107 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONA encoding novel human diagnostic protein #17333
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                                                                                                                                                                                                                                                                           RESULT 6
AAS81529/c
ID AAS81529 standard; cDNA; 406 BP.
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P-PSDB; ABG17342.
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                                                                               2040 CCTG 2043
                                                                                                                                                              1834 CCTG 1837
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1;

Gaps

40;

Best Local Similarity 90.7 Matches 390; Conservative

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5^{\circ}-CpG-3', present in a
                                                                                                          useful
of
                                              2542 CGGGATGGCTGGGAGGCCCCCCACTGCGAGAACCGTGAGTGGAGCTCTTGCTCTGTATGT 2601
                                                                                                                                                                                                                                           2722 TTCTGGAATGTCTGTGCCCCCAGGTCCTTAGAATGTCTGCTTCCGGCGGCGTGGCCAGGACCA 2781
                                                                                                                                                                                                                                                                                                          2782 CTATTCTCACTGAGGGAGGAGGATGTCCCAACTGCAGCCATGCTGCTTAGAGACAAGAAA 2841
                                                                                                                                                                                                                                                                                                                                                                           266 AGCAGCCGTACCCCTCCCAGCAACTACAGAAGGCCTGGGCACTGAAATGGTGCCTACC 207
                                                                                                                                                                                                                                                          Human, cytosine methylation, 5'-CpG-3', uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                           406 AGCCCGTGCATGAATGAGGGCAGCTGCGTGCAGAATGGGAGCTACCGCTGCAAGTGT
                                                                                                                                                                           AGCAGCCGTACCCCTCCCCAGCAACTACAGAAGGCCTGGGCACTGAAATGGTGCCTACC
                                                                                                                                                                                                                                                                                                                             Oligonucleotide for detecting cytosine methylation SEQ ID NO 2699.
                                                               346 CGGGATGGCTGGGAGGGCCCCCACTGCGAGAACC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated {\sf DNA}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
ABQ16108/c
ID ABQ16108 standard; DNA; 651 BP.
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05-SEP-2000; 2000DE-1044543.
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01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543.

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genomic sample of DNA. The sample is treated chemically to convert
CC Sytosine (C) but not methylated C, to uracil, then part of the genomic
DNA that contains the target C is amplified to form a labeled amplicon.
The amplicon is hybridised to two classes, each with at least one
member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
and the degree of hybridisation to both classes is determined from the
clabel on the amplicon. From the ratio of labels hybridised to the two
classes of oligomers, the degree of methylation is calculated. The method
is used (i) for diagnosis and/or prognosis of side effects of
the central nervous, cardiovascular, gastrointestinal and respiratory
systems etc., particularly by detecting mutations or single nucleotide
colymorphisms (SNP's); and (ii) for differentiation of cell or tissue
colymorphisms (SNP's); and (ii) for differentiation of cell or tissue
colymorphisms (SNP's); and (ii) for differentiation of simultaneously.
ABQ13410-ABQ34121 represent genomic DNA sequences used to illustrate the
characteristic of the cardior of the cardior described in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 AGCCGCGCCCCGGGCGCCCCTCCTGTGATCCCGTAGCGCCCCTGGCCCGAGCCGCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 ATACCGCTTTAAAAAACGCGAAAAACTCTATACACCTCCCTAACGATAATTCCTCCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGCCGGGTCGGGTCGTGCCGCCCTCTCCCAGGAGAGAACAGGTGTCCCACGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                           Score 201; DB 24; Length 651;
Pred. No. 8.1e-40;
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                                                                                                                                                                                                                                                                                                                                                         Sequence 651 BP; 112 A; 68 C; 227 G; 244 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Best Local Similarity 76.6%;
Matches 246; Conservative
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ABQ16109
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the lasses of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 ATGCCGCTTTAAAAAACGCGAGGGGCTCTATGCACCTCCCTGGCGGTAGTTCCTCCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGCCGGGTCGGGTCGTGCCGCCCTCTCCCAGGAGACAAACAGGTGTCCCACGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, use for diagnosis and prognosis, comprises selective hybridization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0%; Score 201; DB 24; Length 651; Best Local Similarity 76.6%; Pred. No. 8.1e-40; Matches 246; Conservative 0; Mismatches 75; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 651 BP; 244 A; 227 C; 68 G; 112 T; 0 other;
                                                                                                                                                                                                                                       Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                        Guetig
                                                                                                                                                                                                   amplicons from chemically treated DNA
                                                                                      Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ16106 standard; DNA; 651 BP
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                                                                                      Olek A, Piepenbrock C,
                                                   (EPIG-) EPIGENOMICS AG
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us-09-930-020a-1_1.rng

301

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182 GTCGCGTTTCGGGCGTTTTTTTTTTTTTCGTAGCGTTTTTTGGTTCGAGTCGCGTTCG 241
                                      324 CAACATGCCCCCTTTCCTGTTGCTGGAGGCCGTCTGTGTTTTCCTGTTTTCCA 376
                                                                                                                                    302 TITAGITICGAGITIGGCGITCGGGIAITCGITAGIGICGGTTGTCCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                 ABQ16107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5' cpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C. to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the reactil nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide types and for investigating cell differentiation of cell or tissue cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

The disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                  Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 TGCCGCTTTAAAAAACGCGAGGGGCTCTATGCACCTCCCTGGCGGTAGTTCCTCCGACCT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 CAGCCGGGTCGGGTCGTGCCGCCCTCTCCCAGGAGACAAACAGGTGTCCCACGTGGCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGTCGGGTCGGTCGTCTTTTTTTTTTAGGAGAGATAAATAGGTGTTTTACGTGGTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTCGTTTTTAAAAACGCGAGGGGTTTTTATGTATTTTTTGGCGGTAGTTTTTTCGATTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGCGCCCCGGGCGCCCTCCTGTGATCCCGTAGCGCCCCTGGCCCGAGCCGCGCCGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide for detecting cytosine methylation SEQ ID NO 2697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%; Score 177; DB 24; Length 651; 88.8%; Pred. No. 7.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.8%; Pred. No. 7.4e-34;
tive 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 651 BP; 84 A; 68 C; 228 G; 271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56pp + Sequence Listing; 56pp; German.
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                                                                                                                                                                                                                                                                                                                           01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity vo.v
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                             WO200218632-A2.
12-JUL-2002
                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                   07-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracid, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the classes of oligomers. The degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide colymorphisms (SNP's); and (ii) for differentiation of call or tissue types and for investigating cell differentiation. The method allows the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylation status of many C residues to be determined simu. taneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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of
                                                                                                                                                                                                                                                                                                                                                                        drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                    Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                         Oligonucleotide for detecting cytosine methylation SEQ ID NO 2698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the disclosure of the invention.
ABQ16107 standard; DNA; 651 BP
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                        12-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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Homo sapiens.
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                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                              263
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                                                84 TGCCGCTTTAAAAAACGCGAGGGCTCTATGCACCTCCCTGGCGGTAGTTCCTCCGACCT 143
                                                                                                          531
                                                                                                                                            530 TAGTCGGGTCGTGTCGTGTTTTTTTTTTTGGAGAGATAAATAGGTGTTTTACGGGTA 471
                                                                                                                                                                                                  470 Grcccerrrcancerrrrrrangearrrcanceracerrrrangearreagrccerrce 411
              Gaps
                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                    TCGGAGGCTGGGTGACCCGCGTAGAAGTGAAGTACTTTTTATTTGCAGACCTGGGCCGA
                                                                                             144 CAGCCGGGTCGGGTCGTGCCGCCCTCTCCCAGGAGAGACAAACAGGTGTCCCACGTGGCA
                                                                                                                                                                            GCCGCGCCCCGGGCGCCCCTCCTGTGATCCCGTAGCGCCCCTGGCCCGAGCCGCGCCCG
                                                                                                                                                                                                                         264 GGTCTGTGAGTAGAGCCGCCCGGGCACCGAGCGCTGGTCGCCCCTCCTTCCGTTATAT
                                                                                                                                                                                                                                               useful in
of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatior responsible for genetic disorders or other traits and to assess
             0;
                                                                                                                                                                                                                                                                      324 CAACATGCCCCTTTCCTGTTGCTGGAGGCCGTCTGTGTTTTCCTGTTTTCCA 376
                                                                                                                                                                                                                                                                                           350 TTTAGTTTCGAGTTGGTTTTGGCGTTTCGGGTATTCGTTAGTGTCGGTTGTCGA 298
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          novel human diagnostic protein #27655.
Pred. No. 7.4e-34;
); Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 27655; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                     AAS91851 standard; cDNA; 1491 BP
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 68.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
             Conservative
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P-PSDB; ABG27664.
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity
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  Local
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Matches
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed sepecification, but was obtained in electronic format directly from WIPO
(II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGACATCAAGGCGGCTGTGCGGAATATGTCCTACATGGAGAAGGGCACAATGACTGGGG 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          947 TGGTGCAGTACTCAAGCTCTGTGCGCCAGGAGTTCCCCCTGGGTCGCTTCCACAAGA 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1187 CCAAGAAGGCCAAAGACCTCGGCTTTAAGATGTTTGCTGTGGGGTGTGGGCAATGCCGTGG 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 AAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATGTGGTGCTCGGCTGCAGTGGACA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorder; coronary artery disease; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  887 AGTICATCAGATCGTGGATACGCTGGACGTGTCAGACAAGCTGGCCCAGGTGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTITGCCATCACAGTCTGTGACGGTCTGGACATCAGCCCCGAGAGGGTCAGAGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 TCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGAGCTTTGAAAGGTCCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.9%; Score 98.8; DB 23;
50.8%; Pred. No. 2.6e-14;
Live 0; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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Matches 266; Conservative
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AAXOO664
ID AAYO
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                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during feam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as a therosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotide sequences can also be used useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation.
                                                                                                                                                                                                          Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1308 TGGTGCAGTACTCAAGCTCTGTGCGCCAGGAGTTCCCCCTGGGTCGCTTCCACCAAGA 1367
                                                                                                                                         Mikita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1128 ACAGCGACGCCAAGACCTGCAATGTCTGCAGTGGTGGTGGTGGCGCCACTCGGCCACTGACC 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTICATCAGTCAGATCGTGGATACGCTGGACGTGTCAGACAAGCTGGCCCAGGTGGGGC 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1368 AGGACATCAAGGCGCCTGTGCGGAATATGTCCTACATGGAGAAGGGCACAATGACCGGGG 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 ACTTTGCCATCACAGTCTGTGACGGTCTGGACATCAGCCCCGAGAGGGTCAGAGTGGGAG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 TCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGAGGCTTTGAAAGGTCCAAGC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 CATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAAC 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 AAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATGTGGTGCTCGGCTGCAGTGGACA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776 TGCCCCAGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGCACTGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.9%; Score 97.8; DB 24; Length 4151; Similarity 50.6%; Pred. No. 7e-14; 55; Conservative 0; Mismatches 253; Indels 6;
                                                                                                                                           Porter GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4151 BP; 889 A; 1089 C; 1163 G; 928 T; 82 other;
                                                                                                                                         Seilhamer JJ,
                                                                                                                                                                                                                                                                    Claim 1; Page 84-85; 315pp; English.
                                                                                                                                         Somogyi R, Lawn R,
                                                                               35-APR-2000; 2000US-195106P.
                                                     34-APR-2001; 2001WO-US11128
                                                                                                             (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 265; Conservative
                                                                                                                                                                                 WPI; 2002-010925/01.
WO200177389-A2.
                                                                                                                                      Shiffman D,
                          18-OCT-2001
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Human; secreted protein, fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allery; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthitis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Florence KA;
Ni J, Olsen HS;
                           1608 AGGATGAGCTGAGGAAATAGCCTCAGAGCCTGTGGCAGAGCAC
896 GGGAGGAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCCAGCAC
                                                                                                                                                                                                                                                                                                       Human secreted protein gene 54 clone HE8EM69.
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Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebner R, Ferrie A
Lafleur DW, Moore
Shi Y, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 215-216; 385pp; English
                                                                                                                                                             BP.
                                                                                                                                                           AAX00664 standard; DNA; 1668
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97US-0048099.
97US-0048131.
97US-0048135.
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97US-0048186.
97US-0048187.
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970S-0048350.
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970S-0048355.
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Hu JS,
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Greene JM,
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generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          879 GGTCAGGTTTCCCAGGTGGGAGGAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCAGCA 938
                                                                                                                                                                                                                                               473 CAGTGGACATCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGAGCTTTGAAA 532
                                                                                                                                                                                                                                                                                                 533 GGTCCAAGCACTTTGCCATCACAGTCTGTGACGGTCTGGACATCAGCCCCGAGAGGGTCA
                                                                                                                                                                                                                                                                                                                 819 GGATGTGGCACTGCCATCCAAGCAGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGTGGG
                                                                                                                                                                                                                                                                                                                                                  593 GAGTGGGAGCATTCCAGTTCCACTCCTCCATCTGGAATTCCCCTTGGATTCATTTT
                                                                                                                                                                                                                                                                                                                                                                          381 GAGTGGGGCTGCTCCAGTATTCCACAGGGTCCACAGAGTTCACTCTGAGAAACTTCA
                                                                                                                                                                                                                                                                                                                                                                                                     653 CAACCCAACAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGGGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                               441 ACTCAGCCAAAGACATGAAAAAGCCGTGGCCCACATGAAATACATGGGAAAGGGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       713 AGACGGAACTTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATGCTT
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                                                                                                                                                                                                Length 1668;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                    Sequence 1668 BP; 575 A; 332 C; 372 G; 385 T; 4 other;
                                                                                                                                                                                                                      0; Mismatches 239;
                                                                                                                                                                                              Score 74.6; DB 20 Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA clone (5'-primer) SEQ ID NO:768.
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                                                                                                                                                                                               2.2%;
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                                                                                                                                                                                                           Local Similarity
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polypucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises a fleat 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complance complementary to the complance complementary to the complance compress a 1'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence of sequence of the combination of the 5'-end sequence/3'-end sequence; where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises a selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs represent human amino acid sequences; and AAH13629 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human and of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2018 ACCCTGACGTGACACAGGTCGGCCTGGTGTATGGCAGCCAGGTGCAGACTGCCTTCG 2077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                      Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 782 BP; 145 A; 223 C; 271 G; 140 T; 3 other;
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No. 2.6e-08;
                                                                                                                                                                                                                                                                                                                                                               sogai T, Nishikawa T, Hayashi K, S.
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 768; 2537pp + CD ROM; English.
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Pred.
                                                                                                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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2000EP-0116126
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                                                                                                                                                                                                                                                                                          (HELI-) HELIX RES INST
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Isogai T,
                                                                                                                                                                               02-MAY-2000;
09-JUN-2000;
                                                                                                                                                 11-JAN-2000;
28-JUL-2000;
                                                                        29-JUL-1999;
                                                                                                       27-AUG-1999;
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Ishii S,
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Sequence 1167 BP; 203 A; 337 C; 424 G; 203 T; 0 other;
   of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 -end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                              2249 GCGGGAGAGGCGCAGAGGATGCAGCCGTTCCTGCCCAGAAGCTGAGGAACAATGGCATCT 2308
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
                                                                                                                                                  474 ATGCCGCTCCCAGGATGACATCTCGGTGTGGGCAGCGCGCCCCAAGGAGGAAGGCATCG
                                                                                                                                                                                                                    2309 CTGTCTTGGTCGTGGGCGTGGGGCCTGTCCTAAGTGAGGGTCTGCGGAGGCTTGC 2363
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Wakamatsu A, Nagai K, Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence SEQ ID NO:16503
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH17154 standard; cDNA; 1167 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1999; 99JP-0300253;
11-JAN-2000; 2000JP-0118776;
32-MAY-2000; 2000JP-0183767;
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09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer;
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Ishii S,
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2018 ACCCTGACGTGACACAGGTCGGCCTGGTGTATGGCAGCCAGGTGCAG.CTGCCTTCG 2077
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                                                                                                                         1898 GGTGCCGGACAAGCCCTGGACCTCGTCTTCATGTTGGACACCTCTGCCTCAGTAGGGC 1957
                                                                                                                                                                                                                                         CCGAGAATTTTGCTCAGATGCAGAGCTTTGTGAGAAGCTGTGCCCTCCAGTTTGAGGTGA 2017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 TGGAACGCGCCACCATGACAGGGCTGGCGTTGCGGCCACATGGTGGAGCACACCTTCTCG 413
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                                                               6
         Length 1167;
                                                               Indels
Score 74.2; DB 22;
Pred. No. 3.1e-08;
0; Mismatches 233;
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      2.28;
                                    Best Local Similarity 49.1
Matches 233; Conservative
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Job time: 493 secs
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Sequence 1, Application US/09930020A

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Sequence 1, Application OS US200007756BA1

GENERAL INFORMATION:
APPLICANT: Mack, Dayld H.
APPLICANT: Wark, Dayld H.E.
APPLICANT: Wark Day, Neith E.
TITLE OF INVENTION: Methods of Diagnosis of Colorectal Cancer, Compositions;
TITLE OF INVENTION: and Methods of Screening for Colorectal Cancer;
TITLE OF INVENTION: Modulators
FILE REPRENCE: 018501-003100US

CURRENT FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: US/09/930,020A
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                                                                                                                                                  US-10-137-865-293
US-10-140-474-293
US-09-904-829-33
US-09-909-204-33
US-09-909-204-33
US-10-143-114-293
US-09-906-646-33
US-09-906-646-33
US-09-906-700-33
US-09-907-7498-33
US-09-907-7498-33
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100.0%; Pred. No. 0;
tive 0; Mismatches
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OTHER INFORMATION: CBF9
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Best Local Similarity
Matches 3375; Conserv
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NAME/KEY: CDS
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16080.529 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/NS06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/NS06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/NS08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/NS08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:
                           GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries

    nucleic search, using sw model

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Sy q	241	CCCCTGGCCCGAGCCGCGCGCGGGTTGGAGTAGAGCCGCCGGGCACCGAGCGCTGG 31	00
Oy Dp	301	TCGCCGCTCTCCCTTCCGTTATATCAACATGCCCCCTTTCCTGTTGCTGGAGGCCGTCTGT 31	09
Q.y D.b	361	GTTTCCTGTTTTCCAGAGTGCCCCCATCTCCCCTCTCCAGGAAGTCCATGTAAGCAAA 4.	20
Qy Db	421	GAAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATGTGGTGCTCGGCTGCAGTGGAC 41	. 08
oy D	481	ATCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGAGCTTTGAAAGGTCCAAG 5. 	. 40
Oy Db	541	CACTITICCCATCACAGICIGACGGICIGGACATCAGCCCCGAGAGGGICAGAGIGGGA 6	: 00
Oy Dp	601	GCATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAA 6. 	
O.y Db	661	CAGGAACTGAAGCCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGGAGAGAGA	20
Oy Dp	721	CTTGCTCTGAAATACCTTCTGCAGAGGGTTGCCTGGAGGGAG	. 08
Oy Db	781	CAGATCCTCATCATCATCATCATGGGAAGTCCCAGGGGGATGTGGCACTGCCAAG 8.	40
Oy Dp	841	CAGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGTGGGGGTCAGGTTTCCCAGGTGGGAG	. 00
Oy Db	901	GAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCAGCACGTGCTGTTGGCTGACAGGTG 9-	09
Qy Db	961	GAGGATGCCACCACCACCCACCTCTTCAGCACCCTCAGCAGCTCGGCCATCTGCTCCAGCGCC 1.	020
Oy Dp	1021	ACGCCAGACTGCAGGGTCGAGGCTCACCCTGTGAGCACACGACGCTGGAGATGGTCCGG 1.	080
Oy Db	1081	GAGTTCGCTGGCAATGCCCCATGCTGGAGAACGATCGCGGCGGACCCTTGCGGTGCTGGGT 1	140 140
oy Ob	1141	GCACACTGTCCCTTCTACAGCTGGAAGAGTGTTCCTAACCCACCC	200

1920 1260 1320 1380 1380 1440 1440 1500 1500 1560 1560 1620 1620 1680 1680 1740 1740 1800 1800 1860 1860 1920 1980 1980 2040 2040 2100 2100 2160 2160 2220 2220 2340 GAGCTGCAGGGGAAGCTGTGCAGCCGGCAGCGCCAGGGTGCCGGACACAAGCCCTGGAC GGCAGCCCAAAGCATGTGATGGTCTACTCGGATCCTCAGGATCTGTTCAACCAAATCCCT CTGGTGTGTATGGCAGCCAGGTGCAGACTGCCTTCGGGCTGGACACCAAACCCACCGG GCTGCGATGCTGCGGGCCATTAGCCAGGCCCCTACCTAGGTGGGGTGGGGTTCAGCTCAGCCGGC ACCGCCCTGCTGCACATCTATGACAAAGTGATGACCGTCCAGAGGGGTGCCCGGCCTGGT GCCCAGAAGCTGAGGAACAATGGCATCTCTTTTTTTTGGTCGTGGGCGTGGGCCTTGTCCTA GCCGTGCTGAGCGAGGACTCTCGGGCCCGAGTGGGTGTGGCCCACATACAGCAGGGAGCTG CTGGTGGCGGTGCCTGTGGGGGGAGTACCAGGATGTGCCTGACCTGGTCTGGAGCCTCGAT GGCATTCCCTTCCGTGGTGGCCCCCACCCTGACGGGCAGTGCCTTGCGGCAGGCGGCAGAG GAGCTGCTCCTGCTGGGTGTAGGCAGTGAGGCCGTGCGGGCAGAGCTGGAGATCACA AGCTTTGTGAGAAGCTGTGCCCTCCAGTTTGAGGTGAACCCTGACGTGACACAGGTCGGC TGTGCCCTGAAGCTGAGCCTGGAATGCAGGGTCGACCTCCTCTTCCTGCTGGACAGCTCT GCGGGCACCACTCTGGACGCCTTCCTGCGGGCCAAAGTCTTCGTGAAGCGGTTTTGTGTGCGG 1261 1321 1381 1741 1801 1861 1921 1921 1981 2041 2041 2101 2101 2161 2161 2221 2221 2281 1441 1561 1561 1621 1681 1681 1861 1981 1201 1201 1261 1321 1441 1501 1501 1621 1741 1801 1381 ga . q ОP q qq Qγ qq δλ q δ ŏ 셤 οy g QΥ Q ò QQ δy QQ ŏ g δ СD ò В Ġ. g ŏ qq Ω οy qq δ οy δ Q

SGTCTTC 3375

Db 3361 ACCTTGAAGG	RESULT 2 US-10-152-661-350 ; Sequence 350, Appl	უ. დ	APPLICANT: APPLICANT: APPLICANT: APPLICANT:		; CURRENT FILING DR ; PRIOR APPLICATION ; PRIOR FILING DATE ; PRIOR APPLICATION			PRIOR FILI PRIOR APPL PRIOR FILI NUMBER OF	SOTTWARE: FASTSE; SEQ ID NO 350 LENGTH: 1837	; ORCANISM: Mouse US-10-152-661-350 Query Match	Best Loc Matches	Qy 302 CGCCGCTCTC Db 101 CGCGGCGTCC	Qy 362 TTTCCTGT	Db 161 TGCTCCTGT1	Db 221 AGACCATGGG	281	Qy 542 ACTTTGCCAT	n n	Db 401 CCTTGCAGTT	461
	TTAC 2400 11 TAC 2400	3CAG 2460 - SCAG 2460	SAAT 2520 SAAT 2520	TGAG 2580 11 GAG 2580	SCAC 2640 	2700	crgc 2760 	2820	AGTT 2880 11 AGTT 2880	TCAT 2940 1 FCAT 2940		CTGA 3000 SCAG 3060	1111 SCAG 3060	AGCA 3120 AGCA 3120	3666 3180 3666 3180		3AAA 3240	3AGT 3300 1111 3AGT 3300	STCC 3360	
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																	CTTGAGGGACGTTTGTGACTTCTTGC	GGTCTCAGACTGAATGTGACCAATTR	TGTGCATGGGCCCAGGTCTGGAGGGC	ACCTGAAGGTCTTC 3375
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EWITON: and Methods for Their Use
EE: 11000.101165.
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EE: 2002-05-20

NG DATE: 2002-05-20

BATION NUMBER: 06/221,232

BATION NUMBER: 60/206,650

BATE: 2000-07-25

ATION NUMBER: 09/312,283

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ATION NUMBER: 09/312,283

ATION NUMBER: 09/189,930

BATE: 1999-04-29

ATION NUMBER: 09/189,930

BATE: 1998-04-29

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                                   782 AGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGCCACTGCCATCCAAGC
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                                                   TGAGCTGCAGGGGAAGCTGTGCAGCCGGCAGCGCCAGGGTGCCGGACACAAGCCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 350, Application US/09866050A
Publication No. US20030040471A1
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Steaman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Oncust, Rene
APPLICANT: Murison, James G.
TITLE OF INVENTION: Compositions Isolated From Skin
TITLE OF INVENTION: Compositions Isolated From Skin
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SEQ ID NO 350
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Matches 1392; Conserv
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| CCTG 1837
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US-09-866-050A-350
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Db 1538 GGAGCTACTCCTGGGCGTGGGC QQ 1800 AGGCACCCAAAGCATGTGATGGTC	1598	1656	DD 1716 CCTGGTCTTCATGTTGGACACCTCT	Oy 1980 GAGCTTTGTGAGAAGCTGTGCCCTC	Oy 2040 CCTG 2043	RESULT 4 US-09-984-245-64 ; Sequence 64, Application US/09984	GENERAL INFORMATION: GENERAL INFORMATION: TILLE OF INVENTION: 87 Human Sec	CURRENT APPLICATION NUMBER: US/O CURRENT FILING DATE: 2001-10-29 PRIOR APPLICATION NUMBER: 09/154	FRIOR FILING DATE: 1998-09-1/ PRIOR APPLICATION NUMBER: DCT/US PRIOR FILING DATE: 1998-03-19 PRIOR APPLICATION NUMBER: US 60/		PRIOR FILING DATE: 1997-03-21 PRIOR PILING DATE: 1997-03-21 PRIOR FILING DATE: 1997-03-21 PRIOR PELLON NUMBER: 05 60/			PRIOR FILING DATE: 1997-05-30 PRIOR PILING DATE: 1997-05-30 PRIOR PILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/	PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/ PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US 60/	PRIOR FILING DATE: 1997-03-30 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-05-30 PRIOR APPLICATION NUMBER: US PRIOR APPLICAT	PRIOR FILING DATE: 1997-03-30 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-05-30 PRIOR PILING DATE: US PRIOR APPLICATION NUMBER: US PRIOR PRICE NAME 1002-05-30	
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	722 TTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATGCTTCTGTGCCCC 781 1 1 1 1 1 1 1 1 1 1 1 1 1	782 AGATCCTCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGCACCTGCCATCCAAGC 841	842 AGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGGGGGGTCAGGTTTCCCAGGTGGGAGG 901		962 AGGATGCCACCACGGCCTCTTCAGCACCTCAGCAGCTCGGCCATCTGCTCCAGCGCCA 1021	1022 CGCCAGACTCCAGGGTCGAGGCTCACCCCTGTGAGCAGGAGGACGTGGAGATGGTCCGGG 1081	1082 AGTTCGCTGGCAATGCCCATGCTGGAGAGGATCGCGGGCCGTTGCGGTGCTGGCTG	1142 CACACTGTCCCTTCTACAGCTGGAAGAGTGTTCCTAACCCACCC	1202 GGACCACCTGCCCAGGCCCCTGTGACTCGCAGCCCTGCCCAGAATGGAGGCACATGTGTTC 1261 1111 111	1262 CAGAAGGACTGGACCGCTACCAGTGCCTCTGCCCGCTGGCCTTTGGAGGGGGGGG	1322 GTGCCCTGAAGCTGAACCTGGAATGCAGGTCGACCTCCTCTTCCTGCTGGACGCTCTG 1381 	1382 CGGCCACCACTCTGGACGGCTTCCTGCGGGCCAAAGTCTTCGTGAAGCGGTTTGTGCGGG 1441 	1442 CCGTGCTGAGCGAGCACTCTCGGGCCCGAGTGGGTGGCCACATACAGCAGGGGGCTGC 1501 	1502 TGGTGGCGGTG-CCTGTGGGGGAGTACCAGGA-TGTGCCTGACCTGGTCTGGAGCCTCGA 1559 	1560 TGGCATTCCCTTCGTGGTGGCCCCACCTGACGGCAGTGCCTTGCGGCAGGCGGCAAA 1619 1111111111111111111111111111111111	1620 GCGTGGCTTCGGGAGCGCCACCAGGACAGGCCACGGCCACGTAGAGTGGTGGTTTT 1679 	1680 GCTCACTGAGTCACACTCCGAGGATGAGGTTGCGGGCCCAGGCGCGTCACGCAGAGGCGCG 1739 1478 GCTCACTGAATCACGCTCCCAGGATGAGGTCTCTGGGCCAGCAGCAGCACGCAAGGCTCG 1537	1740 AGAGCTGCTCCTGCTGGGTGTAGGCAGTGGGGGGGGGGG
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CAGTGAGATCCTGCAGGCGGAGCTGGTGAAGATCAC 1597
                                          3CCGGCAGCGCCAGGGTGCCGGACACAAGCCCTGGA 1919
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APPLICATION NUMBER: PCT/US98/05311

FILING DATE: 1998-09-17

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321 TCGTGAAGCAGTTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTC 380
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Pred. No. 1.1e-11;
0; Mismatches 239;
PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR PELICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-08-05
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR PRICATION NUMBER: US 60/056,872
PRIOR APPLICATION NUMBER: US 60/050,862
PRIOR PRIOR DATE: 1997-11-02
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US-09-984-245-64
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Best Local Similarity 48.9%;
Matches 242; Conservative
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SEQ ID NO 64
LENGTH: 1668
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ORGANISM: Homo sapiens
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Sequence 64, Application US/09966262
Publication No. US20030050461A1
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1

us-09-966-262-64

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CAGTGGACATCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGAGCTTTGAAA 532
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Pred. No. 1.1e-11;
0; Mismatches 239;
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PRIOR APPLICATION NUMBER: US 60/048,154
PRIOR PILLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR APPLICATION NUMBER: US 60/056,370
                                APPLICATION NUMBER: US 60/042,344 FILING DATE: 1997-03-21 APPLICATION NUMBER: US 60/042,344 APPLICATION NUMBER: US 60/041,276
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,099
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,352
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,095
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PRIOR APPLICATION NUMBER: US 60/048,096
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,355
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PRIOR APPLICATION NUMBER: US 60/048,160
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,351
PRIOR FILING DATE: 1997-05-30
                                                                                                                  FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,281
                                                                                                                                                       FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/048,094
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APPLICATION NUMBER: US 60/048,188
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/048,135
                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-05-30 APPLICATION NUMBER: US 60/050,937
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APPLICATION NUMBER: US 60/048,187
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; OTHER INFORMATION: n equals a,t,g, or
US-09-966-262-64
                                                                                                                                                                                                                APPLICATION NUMBER: US 60/048,350
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Best Local Similarity 48.9%;
Matches 242; Conservative
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LING DATE: 1998-03-19
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SEQ ID NO 64
LENGTH: 1668
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939 CGTGCTGTTGGCTGA 953
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533 GGTCCAAGCACTTTGCCATCACAGTCTGTGACGGTCTGGACATCAGCCCCGAGAGGGTCA 592
                                              321 TCGTGAAGCAGTTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTC 380
                                                                                                                                            381 GAGTGGGGCTGCTCCAGTATTCCACACAGGTCCACAGAGTTCACTCTGAGAACTTCA 440
                                                                                                                                                                                             653 CAACCCAACAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGG 712
                                                                                                                                                                                                                                         441 ACTCAGCCAAAGACATGAAAAAGCCGTGGCCCACATGAAATACATGGAAAAGGGCTCTA 500
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                                                                                              593 GAGTGGGAGCATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
CURRENT APPLICATION NUMBER: US/09/983,966
CURRENT FILING DATE: 1908-09-17
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1997-03-21
PRIOR PELING DATE: 1997-03-21
PRIOR PRIOR APPLICATION NUMBER: US 60/041,277
PRIOR PELING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041,281
PRIOR APPLICATION NUMBER: US 60/048,094
PRIOR PELING DATE: 1997-03-30
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,187
PRIOR PLING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
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Publication No. US20030060619A1
GENERAL INFORMATION:
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2.2%; Score 74.6; DB 9;
Best Local Similarity 48.9%; Pred. No. 1.1e-11;
Matches 242; Conservative 0; Mismatches 239:
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,095
PRIOR FILING DATE: 1997-05-30
PRIOR PLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048,131
PRIOR FILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
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PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/054,804
PRIOR PELING DATE: 1997-08-05
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LOCATION: (1664)
OTHER INFORMATION: n equals a,t,g, or
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SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
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2081 TCGTGAAGCAGTTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTC 2140
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                         APPLICANT: Fernandes, Elma
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING 5
FILE REFERENCE: 15966-556
CURRENT PELICATION NUMBER: US/10/000,512
CURRENT FILING DATE: 2001-10-23
PRIOR PAPLICATION NUMBER: 09/619,252
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 1909-11-29
NUMBER: OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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Pred. No. 2.8e-11;
0; Mismatches 239;
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        APPLICANT: Shimkets, Richard A
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Best Local Similarity 48.8%;
Matches 242; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Bestelin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (55)..(2931)
US-10-000-512-9
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                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3447
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APPLICANT:
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Pred. No. 1.1e-11;
0; Mismatches 239;
                                                                                                                       Sequence 54, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
APPLICANT: YOUNG et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REPERENCE: PS004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILIANG DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PETCHING DATE: 100 64
LENGTH: 1668
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US-10-143-090-64
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Patent No. US20020164699A1
GENERAL INFORMATION:
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Matches 242; Conservative
741 TCTCTTCTATGCCGA 755
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US-10-000-512-9
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2098 TCGTGAAGCAGTTTGTCACGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTC 593 GAGTGGGAGCATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTT

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2278 TGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCA 2337

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713 AGACGGAACTTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATG--- 769

770 ------CTTCTGTGCCCCAGATCCTCATCGTCACTGATGGGAAGTCCCAGG

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2218 ACTCAGCCAAAGACATGAAAAAGCCGTGGCCCACATGAAATACATGGGAAAGGGCTCTA 2277

653 CAACCCAACAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGG

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/905,291A

CURRENT FILING DATE: 2001-07-12

PRIOR PAPLICATION NUMBER: PCT/US00/04414

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PRILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-08

PRIOR PRILICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-112-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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FILING DATE: 1999-12-02
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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                                                  Gao, Wei-Qiang
Gerber, Hanspeter
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Filvaroff, Ellen
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ORGANISM: Homo sapiens
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2518 ATCTCTTCTATGCCGA 2533

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878 GGGTCAGGTTTCCCAGGTGGGAGCAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCAGC 937

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818 GGGATGTGGCACTGCCATCCAAGCAGCTGAAGGAAAGGGGTGTCACTGTTTGLTGGTGG

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,853
CURRENT FILING DATE: 2000.07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR FILING DATE: 2000-09-18
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
                  Sequence 33, Application US/09902853 Publication No. US20020192659A1
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Grimaldi, Christopher Gurney, Austin L.
Hillan, Kenneth, J.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Mather, Jennie P.
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                                                                                  APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Gao, Wei-Qiang
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                                                           GENERAL INFORMATION
US-09-902-853-33
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APPLICANT:
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APPLICATION NUMBER: PCT/US99/28565
                                                                                                    FILING DATE: 1999-09-13
PPPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-18
APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/28313
                       FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
                                                        FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/USOO/00219
FILING DATE: 2000-01-05
ION NUMBER: US 60/146,222
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; ORGANISM: Homo Sapien
US-09-902-853-33
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Best Local Similarity
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/907,824
CURRENT FILING DATE: 2001-07-17
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APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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APPLICATION NUMBER: 09/665,350
FILING DATE: 2000-09-18
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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Kljavin, Ivar J.
Mather, Jennie P
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878 GGGTCAGGTTTCCCAGGTGGGAGGAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCAGC 937
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art, Timothy A.
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Matches 242; Conservative
                                                                    Tumas, Daniel
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CORGANISM: Homo sapiens
US-09-907-841-33
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                                                                    APPLICANT
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                                                                                                                                              Length 3449;
                                                                                                                                             Score 73.6; DB 9; Length 3.
Pred. No. 2.8e-11;
0; Mismatches 239; Indels
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Publication No. US20020198366A1
GENERAL INFORMATION:
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                              Query Match 2.2%;
Best Local Similarity 48.8%;
Matches 242; Conservative
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                              TYPE: DNA ORGANISM: Homo Sapien US-09-907-824-33
                                                                                                                                             Query Match
Best Local Similarity
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                                                SEQ ID NO 33
LENGTH: 3449
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APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT APPLICATION NUMBER: US/09/907,841
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-10-05
PRIOR FILING DATE: 1999-10-10-05
PRIOR FILING DATE: 1999-10-10-05
PRIOR FILING DATE: 1999-11-29
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48.8%; Pred. No. 2.8e-11;
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PRIOR APPLICATION NUMBER: PCT/US99/30911
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US-10-028-072-293
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: PCT/USO0/04414
FILING DATE: 2000-02-22
PPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: PCT/US99/28313
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FILING DATE: 1999-12-16
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FILING DATE: 1999-12-02
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APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: 09/665,350
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Grimaldi, Christopher J.
                                                                                                                                                Sequence 33, Application US/09904011 Publication No. US20030003530A1 GENERAL INFORMATION:
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Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
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Hillan, Kenneth, J.
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Gerritsen, Mary E
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                      2518 ATCTCTTCTATGCCGA 2533
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                                          938 ACGTGCTGTTGGCTGA
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US-09-904-011-33
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2158 GAGTGGGGCTGCTCCAGTATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCA 2217
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                                                                                                                                                                                                                                                                                                                               0; Mismatches 239;
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Pred. No. 2.8e-11;
                 PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-112-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 33
LENGTH: 3449
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o. US20030004311A1
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1999-12-20
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Filvaroff, Ellen
Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                                                                          Matches 242; Conservative
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                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo Sapien
US-09-904-011-33
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Publication No. US20
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/028,072 CURRENT FILING DATE: 2001-12-19
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                                                          CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
                                                                                                                                                 APPLICATION NUMBER: 60/059113
FILING DATE: 1997-09-17
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NUMBER: 60/059117
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FILING DATE: 1997-09-17
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NG DATE: 1997-09-18
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1997-09-19
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
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1997-10-24
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FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
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NG DATE: 1997-10-29
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APPLICATION NUMBER: 60/063755
FILING DATE: 1997-10-17
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FILLING DATE: 1997-11-03
APPLICATION NUMBER: 60/064809
FILING DATE: 1997-11-07
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1997-09-17
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NG DATE: 1997-10-29
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FILING DATE: 1997-11-21
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ITLE OF INVENTION:
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R PILING DATE: 1997-12-11

R APPLICATION NUMBER: 60/069694

R FILING DATE: 1997-12-16

R APPLICATION NUMBER: 60/07320

R FILING DATE: 1998-01-23

R APPLICATION NUMBER: 60/073612

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R APPLICATION NUMBER: 60/074086

R APPLICATION NUMBER: 60/074086

R FILING DATE: 1998-02-09 R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066511
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066770
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R APPLICATION NUMBER: 60/069212
R FILING DATE: 1997-12-11 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09
FILING DATE: 1998-04-09
FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081818 APPLICATION NUMBER: 60/074092 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/077791 FILING DATE: 1998-02-27 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/078910 APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082999 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/086430 APPLICATION NUMBER: 60/069278 FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069334 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-04-24 APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/084600 APPLICATION NUMBER: 60/085149 FILING DATE: 1998-05-12 APPLICATION NUMBER: 60/085323 APPLICATION NUMBER: 60/086414 APPLICATION NUMBER: 60/084627 APPLICATION NUMBER: 60/085579 APPLICATION NUMBER: 60/085697 ILING DATE: 1998-03-12 998-05-07 1998-05-15 1998-05-07 LING DATE: 1998-05-1 998-05-- 40-866 -50-866 1998-05-LING DATE: LING DATE: LING DATE: LING DATE: PRIOR PRIOR

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2098 TCGTGAAGCAGTTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCGCAAAGCCGCTC 2157
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Pred. No. 2.
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088730
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APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091360
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Best Local Similarity 48.8%;
Matches 242; Conservative
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PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1999-09-08
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FLIING DARTE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
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FILING DATE: 1999-12-20
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Grimaldi, Christopher J.
                                                                                                                                                Sequence 33, Application US/09906742 Publication No. US20030023054A1
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Gao, Wei-Qiang
Gerber, Hanspeter
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                                       2518 ATCTCTTCTATGCCGA 2533
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Ashkenazi, Avi
Botstein, David
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aton, Dan L
938 ACGTGCTGTTGGCTGA
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Pred. No. 2.8e-11;
0; Mismatches 239; Indels 15;
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Best Local Similarity 48.8%;
Matches 242; Conservative
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GORGANISM: Homo Sapien
US-09-906-742-33
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LENGTH: 3449
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BJ09333 BJ499393

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AJ395774 BJ39509.9

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BJ067406 BJ067406

AJ39677411 BB577711

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AK01753 MUS MUSCURT

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BBD16450 BBB164450
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1024)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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Plate: LLAM9272 row: m column:
High quality sequence stop: 667.
Location/Qualifiers
1. 1024
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AV607535
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AV595999
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BO78029
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BJ003847
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BJ036168
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BJ08618
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BJ18
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BB577711
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BQ876319
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AV592803
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BF849816 PM4-EN006
BB617396 BB617396
AZ34444 IM0078P24
BB613951 BB613951
AW206492 UI-H-BII-
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18171.465 Million cell updates/sec
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                 GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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12.7
11.6
11.5
10.4
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Minimum DB seq Maximum DB seq

Jatabase

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

source

FEATURES

458.8 428.6 393 389.8 349.4 340

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                  /db_xref="taxon:10090"
/clone="IMAGE:4019899"
/clone=lib="WOI_CGAP_LN29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DHIOB"
/note="Organ: lung, Vector: pCMV-SPORT6; Site_1: SalI:
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
13 a 299 c 330 g 151 t lothers
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                                                                                                                                                                                Score 458.8; DB 12;
Pred. No. 2.6e-100;
                                                                                                                                                                                                         148;
                                                                                                                                                                                                        0; Mismatches
/organism="Mus musculus"
/strain="CZECH II"
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RESULT

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/organism="Homo sapiens"
//organism="Homo sapiens"
//organism="texon:9606"
//organism="Adult"
//organism="texon-goods"
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EST 16-JAN-2001
                                      mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                 Catarrhini; Hominidae;
                                      sapiens cDNA,
                                                                                                                                                                                                                                                                                              Vertebratá;
linear
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    mRNA
                                                                                                                                                                                                                                                                                              Craniata;
BF849816 535 bp mRN
PM4-EN0068-151100-004-b06 EN0068 Homo
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                                                                                 BF849816
BF849816.1 GI:12236966
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Proc. Natl. Acad. Sci.
20202663
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Mammalia; Eutheria;
1 (bases 1 to 535)
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/organism="Mus musculus"

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URL: http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
penese Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 664)
Arakwa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okado, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, Y., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,Y. and Hayashizaki,Y. Computer based methods for the mouse full-length cDNA. Computer based methods for the mouse clustering for construction of a encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawal,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                            BBG17396 664 bp mRNA linear EST 26-OCT-2001
BBG17396 RIKEN full-length enriched, 11 days pregnant adult female
Ovary and uterus Mus musculus cDNA clone 5031412M06, mRNA seguence-
BBG17396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Evkunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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                                                                                                                                                    3258 GACCAATTAACCAGCTTGGTTGATGATGGGGGAGGGGCTGAGTTGTGCATGGGCCCCAGGT 3317
                                                295 CAGAGACATTCTGGATGCATTGCATTGAGTCTGAAAGGGGGCCTTGAGGGACGTTGTGA 236
                                                                                                                                                                                                                                                         3318 CTGGA-GGGCCACGTAAAATCGTTCTGAGTCGTGAGCAGTGTCCACCTTGAAGGTCTTC 3375
                                                                                                                                                                                                                                                                                    RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Location/Qualifiers

mouse tissues Location 1. .664

source

FEATURES

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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. Ist strand cDNA was
primed with a primer [5]
           /clone_lib="RIKEN full-length enriched, 11 days pregnant adult female ovary and uterus" /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 AGACCATGGGGAAGATCGCTGTGGCCAGCAAATTAATGTGGTGCTCAGCCGCGGTCGACA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITICCIGITITICCAGAGIGCCCCCATCICCCTCTCCAGGAAGICCATGTAAGCAAAG 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAAC 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       842 AGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGTGGGGGTCAGGTTTCCCAGGTGGGAGG 901
                                                                                                                                                       /note-"Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 393; DB 10; Length 664;
Pred. No. 2e-84;
0; Mismatches 130; Indels 3
                                                                                   /tissue_type="ovary and uterus"
/dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
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/clone-"5031412M06
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11.6%;
Best Local Similarity 78.4%;
Matches 484; Conservative C
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BB613951
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                                                                                                                                                                                          AZ34444 632 29-SEP-2000 1M0078P24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0078P24 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 632)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
588 AGCTGAGAAAGGGGCATCGTCGTGTTTGCCGTAGGAGTCCGTTTTCCCAGGTGGGACG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGCIM0078P24"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 389.8; DB 17; Length 632; Pred. No. 1.1e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: P column: 24
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 632.
Location/Qualifiers
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83.1%;
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                                       902 AGCTGCATGCACTGGCC 918
                                                              AGCTGCTCACGCTGGCC 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
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Fax: 801 585 7177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 638)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Mateyuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
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Muramatsu, M. and Hayashizaki, Y., et al. 2001)
Unpublished (2001)
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The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
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                                                       CCAGGGTGCCGGACACAAGCCCTGGACCTCGTCTTCATGTTGGACACCTCTGCCTCAGTA 1953
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Gaps
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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URL:http://genome.gsc.riken.gc.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FIG I "
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             Query Match 10.4%; Score 349.4; DB 10; Length 638; Best Local Similarity 78.4%; Pred. No. 7.5e-74; Matches 432; Conservative 0; Mismatches 116; Indels 3;
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/organism="Mus musculus"
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/clone="4832416E03"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Inxace:721001"
/clone="Inxace:721001"
/clone="Inxace:721001"
/clone="Inb="NoT_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
/l
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Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NGI-GAP clone distribution information can be found through the www-bio.llnl.gov/Dbrp/Image.html

Seq primer: M13 Forward
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1. (bases 1 to 406)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781
                                                                                                                          330 GCTTCGCCATCGCTGCCTGTGATGCCCTGGACATCAGCCCTGGCAGGGTCAGAGTCGGAG 389
                                                                                                                                                                                                                                                                         AGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGCACTGCCATCCAAGC 841
       270 TCCTGTTTCTGTTAGATGGCTCTCACAGCATCGGGAAGGGGGAGCTTCGAGAGGTCCAAGC 329
                                                                                                                                                                                                                                                                                                                                                                                        662 AGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGGAGACGGAAC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATGCTTCTGTGCCCC
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TITLE
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NCI_CGAP_LN19, NCI_CGAP_CG4, NCI_CGAP_CG5

NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI_CGAP_KN13 pool 1 LLAM 334-337, 3682-3683,
3798-3803 (IMAGE CloneIDs 132376-132391, 1456008-1456775, 1500552-150285); NCI_CGAP_KN45 pool 1 LLAM 338-3342, 3776-3725, NCI_CGAP_KN45 pool 1 LLAM 338-3342, 3776-3725, NCI_CGAP_KN45 pool 1 LLAM 3164-147901, 1471368-1472903, 1492104-1493255); NCI_CGAP_LOS pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 127096-128631, 1469064-1470983, 1475592-1476743); NCI_CGAP_PCIONEIDS 12706, 3733-3735 (IMAGE CloneIDS 12706, 12706); NCI_CGAP_CG10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDS 1057416-106125, 1144584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon 6 Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research
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                              NCI_CGAP_Lei2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2602 GTGAGCCAGGGATGGATTCTTGAGACGCCCCTGAGGCACATGGCTCCCGTGCAGGGGC 2661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 AGCCCGTGCATGAATGAGGGCAGCTGCGTCCTGCAGAATGGGAGCTACCGCTGCAAGTGT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 40;
NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_CO8, NCI_CGAP_CLL1, NC NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 CGGGATGGCTGGGAGGCCCCCACTGCGAGAACC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.1%; Score 340; DB 10; 190.7%; Pred. No. 1.1e-71; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_LIB-NCI_CGAP_Col0
TAG_TISSUE=colon
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112 c 1
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Matches 390; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 64)?
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sano,H., Sasaki,D., Shibata,K., Shinaqawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (II), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer based methods for the mouse full-length, CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Layashizaki,Y. Computational Analysis of Full-Length Mouse CDNAS Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEMAIL: genome-resegsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
appense. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshhide Hayashizaki
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
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/dev_stage="9 days embryo"
/lab_host="DH10B"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/clone="D030048B17"
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   BB655280 'BB655280.1 GI:16489108
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Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases; Lto 631)

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6 (harea; Lto 631)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
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pBluescript KS(+) after bulk excision from Lambda FLC I." 179\ c 201\ g 129\ t
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                                                                               Length
                                                                             Score 303.8; DB 10; Length
Pred. No. 9.1e-63;
0; Mismatches 147; Indels
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Best Local Similarity 73.4%;
Matches 416; Conservative
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Flease visit our web site (http://genome.goc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1700, H.; Fukunishi, Y.; Shibata, K.; Itoh, M.; Carninci, P.; Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gs.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
appense. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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nces Center(GSC), Yokohama Institute
Institute of Physical and Chemical Research (RIKEN)
22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
81-45-503-9222
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/db_xref="taxon:10090"
/clone="402422118"
/clone_lib="RIKEN full-length enriched, 15 days embryo
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0; Mismatches 105;
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/dev_stage="15 days embryo"
/lab_host="DH10B"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Buses 1 to 420)

RS Almura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiranoto,K., Hiraoka,T., Hirzozane,T. Imchani,K., Ishli,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Salto,R., Sakai,C., Sakai,K., Sakazune,N., Sasaki,D., Sato,K.,
Shibata,K., Shinaqawa,A., Shiraki,T., Sogabo,Y., Suzuki,H., Taqawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ar EST 26-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
"S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 GCTTCGCCATCGCTGTGATGCCCTGGACATCAGCCCTGGCAGGGTCAGAGTCGGAG
                                                                             | ||||| ||||||||| | | | ||||||||| | AGACCATGGGGAAGATCGCTGGCCAGCAATTAATGTGGTGCTCAGCCGGGTCGACA
                                                                                                                                                                                                                                               ACTITGCCATCACAGTCTGTGACGGTCTGGACATCAGCCCCGAGAGGGTCAGAGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                            CCTTGCAGTTTGGTTCCACTCCTCATCTGGAATTCCCCTTGGACTCCTTCTAACTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGGAGACGGAAC
TGCTCCTGTTCTTCAGAGTGTCCCCGACCATCTCTTTCAGGAAGTGCATGTGAACCGGG
                                                   AAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATGTGGTGGTGGTGGTGCAGTGGACA
                                                                                                                                                TCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGAGCTTTGAAAGGTCCAAGC
                                                                                                                                                                                                                                                                                                                                                 602 CATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722 TTGCTCTGAAATACCTTCTGCACAGAGGGTTGCCTGGAGGCAGAAATGCTTCTGTGCCC
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Contact: Yoshihide Hayashizaki
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/clone_lib="RIKEN full-length enriched, adult male kidney"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of nonrequidant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AGGTGGGCGCACCGAGGGCCTAGCCCTGAAA - - - CGCCTGAGCAGAGGGTTCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCAGAAATGCTTCTGTGCCCCCAGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGG
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373996 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF606846.1 GI:11707864
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llarity 80.3%; Pred. No. 3e-53;
Conservative 0; Mismatches 78;
                                                                                                                                                                                                                                                 /organism="Mus musculus"
.Y. and Hayashizaki,Y.
Computer-based methods for the
                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="F530004C06"
                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="kidney"
/dev_stage="adult"
                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                        e mouse tissues.
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BE143292
BE143292.1 GI:8606013
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                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904 e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                     1 (bases 1 to 393)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasse, W. Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle." 76 t
                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GGCCGGAGAACTTCGCCCAGATGCAGAGCTTCGTGAGAAGCTGTGTCCTCCGGTTTGACG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 TGAACCCCGATGTGACGCAGATCGGTCTGGTGTACGCCACCCGTGTCCAGACAGCCT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 57 row: K column: 1
Seq primer: ATTTAGGTGACACTATAG.
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FORWARD: AGGAAACAGCTATGACCAT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 287)

1 (bases 1 to 287)

1 bias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone_lib="HT0161"
/dev_arge="Adult"
/dev_arge="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
Site_1: SmaI; A mini-library was made by cloning products
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=MRO-HT0161-221
099-002-c08&t3=1999-10-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence start: 8
High quality sequence start: 8
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3086 ACGCCGAAGCCCACGCCTTTCAAGATGGAAAGCAGCAGTTTTCCACTTCCCCAGAGAC 3145
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                                                                                                                                                                                                                                                                                                                                                                                                   sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
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2361 IGCAGGICCCCGGGAITCCCTGAICCACGIGGCAGCITACGCCGACCTGCGGIACCACCA 2420
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AW856235.1 GI:7951928
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E (bases 1 to 629)

S Kohara, Y., Shin-i.T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab

Unpublished (2001)

Context: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
                                 BJ003847 F01SSA cDNA Oryzias latipes cDNA clone MF01SSA052D08 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AGTCAAGCTGAGCCTAGGATATTGGACCTGACAAGGTCCGAGTGGGTCTGATTCA 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.2%; Score 176.4; DB 13; Length 629; 60.0%; Pred. No. 8.1e-32; Live 0; Mismatches 206; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MF01SSA052D08"
/clone_lib="MF01SSA cDNA"
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/tissue_type="whole embryo"
/dvs.tage="segmentation stage 20
I63 c 171 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain-"Hd-rR"
                                                                                                    BJ003847.1 GI:17358244
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                                                                                                                                      Japanese medaka
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                                                                   mRNA sequence.
BJ003847
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                               LOCUS
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JOURNAL
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KEYWORDS
SOURCE
RESULT 12
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1...201
//organism="Homo sapiens"
/db_xref="taxon:966"
/db_xref="taxon:966"
/clone_lib="CT0286"
/dev_stage="Adult"
/note="Organ: colon; Vector: pucl8; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 from the pUC 18 vector. Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Cargai, M.R., Matsikuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-270001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=RC1-CT0286-050
400-018-038513=2000-04-05&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 200.
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                                                                                                                                                                                                                                                                                            AW856235 201 bp mRNA linear EST 19-MAY-2000 RC1-CT0286-050400-018-e03 CT0286 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2301 TGGCATCTCTGTCTTGGTCGTGGGCGTGGGGCCTGTCCTAAGTGAGGGTCTGCGGAGGCT 2360
527 AAAATACATCTTGAGGAAGGGTTTTCCGGGTGGCCGTAACTCCTCCAGCGTGCCCCGCAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                              628
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                                                                                                   786 CCTCATCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 t
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69 c 54 q
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2675 CTCCCAGCAACTACAGAGAAGGCCTGGGCACTGAAATGGTGCCTACCTTCTGG 2727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa
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Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery.
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/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dr primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). # 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 438)
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Pred. No. 6.2e-17;
0; Mismatches 118; Indels
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Context: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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/db_xref="taxon:8355"
/clone="XL018k07"
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Location/Qualifiers
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illarity 60.7%;
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/ursue_type="taxon:9606"
/clone_lib="ursuc.19606"
/clone_lib="ursuc.19606"
/clone_lib="ursuc.19606"
/clone_lib="ursuc.19606"
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/dab_host="bH10B (Life Technologies) (Tl phage resistant)*
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR is Site_l: Not I;
/ursuc.ed according to Bonaldo, Lennor and Soares,
constructed according to Bonaldo, Lennor and Soares,
Gonome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, disested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is contained by National Eye Institute (NEI)."
       EST 28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Bonaldo,M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                            L. (Lagra, F. L., Lennon, G. and Soares, M.B. Bonalido, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2615 GGATTCTTGAGACGCCCCTGAGGCACATGGCTCCCGTGCAGGAGGGCAGCAGCGGTACCC 2674
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BM702190 723 bp mRNA lineer EST 28-
UI-E-CQ1-aey-m-08-0-UI.rl UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-aey-m-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 353-608, >LINE2
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Program for Rat Gene Discovery and Mapping
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11arity 100.0%; Pred. No. 2.2e-16;
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Search completed: May 5, 2003, 04:53:50 Job time : 3030 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nı	OM nucleic - nucleic search, using sw model
Rún on:	<pre>May 5, 2003, 04:52:36 ; Search time 5744 Seconds</pre>
Title: Perfect score:	US-09-930-020A-1 3375

1 gacagtgttcgcggctgcac......tgtccaccttgaaggtcttc 3375 Scoring table: Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0

4109280 Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Word size : Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

em_fun: em_or: em_mu: em_om: em_pat GenEmbl:* Database :

Pred. No. is the number of results predicted by chance to have a

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AC305383 Homo sapi AC022023 Homo sabi	AL161942 Homo sapi	G50805 SHGC-83858	AF243083 Homo sapi	AF034611 Homo sapi	ACU5//4/ HOMO Sapi	X80115 H.sapiens N	U77493 Human Notch	AJ406936 Homo sapi	AF308601 Homo sapi	AR102329 Sequence	AX357059 Sequence	AF315356 Homo sapi	AL512503 Human DNA	ALS92545 Mouse DNA	AC025904 Homo sapi	AC025241 Homo sapi	AC095873 Rattus no	AC107303 Homo sapt	AC129682 Rattus no	U	AC11304/ Rattus no	AC025904 Homo sap1	AC113703 Rattus no	AC115294 Mus muscu	3	AF300613 Gallus ga	- c	sap	300606 Human Hp2 g	Chimpanzee	Human	Human ha	3 Homo			A linear FRI 31-OCT-1998 875K-1144G6 mar 10025.1,					ertebrata; E	ги; ноштиллае; ношо.		•
SUMMARIES	DB ID	9 AC005383 9 AC022023	7	11	9 6	σ (ט כ	9 00	9 HSU77493	ת ס	9 AF308601	9	6	o م	9 AL512503	20	· ~	~	~ ~	4 (7	ο, c	40	2	٦ رم	v ~	~	ъ.	40	0	6	9 CHPHAPGC	O UTMUDADE	9	9 AC1048	ALIGNMENTS		123110 bp DNA chromosome 10 clone CIT9875		:3818355	ì			Primares; 10)		numan ciii omosome 10
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/clone_lib="RPCI-11"
48686 a 32379 c 32258 g 47097
                                                                                                                                                                                                                                                                                                                                                             1. .160420
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/db_xref="taxon:9606"
/chromosome="10"
                                                Mammalia; Eutheria; Primates; 1 (bases 1 to 160420) Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-411P18"
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                                                                                                          Sequence Data
                  Homo sapiens.
                              Homo sapiens
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                                                                                                       Direct Submission
Submitted (31-OCT-1998) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02154, USA
On Oct 31, 1998 this sequence version replaced gi:3808081.
                                      Direct Submission
Submitted (05-AUG-1998) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02154, USA
J (bases 1 to 123110)
Smith, D.R.
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Homo sapiens chromosome 10 clone RP11-411P18, complete seguence.
ACO22023
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                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosone="10"
/map="10925.1"
/clone="CIT9875K-1144G6"
/d a 28668 c 29634 g 33413 t
                                                                                                                                                                                                                                                                                   17.5%; Scor.
100.0%; Pred. No. v.
0; Mismatches
                                                                                                                                                            Location/Qualifiers
1. .123110
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             2 (bases 1 to 123110)
Smith, D.R.
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Best Local Similarity
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DEFINITION
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AC022023/c
                        AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                      BASE COUNT
JOURNAL
REFERENCE
                                                                                                         TITLE
JOURNAL
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                                                                                REFERENCE
                                                                                              AUTHORS
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Homo sapiens chromosome 20 clone RP11-83B5, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.

ALL61942.5 GI:9931708
HTG: HTGS_PHASE1; HTGS_CANCELLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submission Submitted (17-MAY-2002) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA On May 17, 2002 this sequence version replaced gi:14522958.

Location/Qualifiers
                                                                                                                                                                                                                                                                                Direct Submission
Submitted (25-JAN-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
3 (bases 1 to 160420)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            Genome Therapeutics Corporation Sequencing Center: Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (22-JUN-2001) Genome Therapeutics Corporation, 100
Street, Waltham, MA 02453, USA
4 (bases 1 to 160420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5193 CAAACAGGTGTCCCACGTGGCAGCCGCCCCGGGGGCGCCCTCCTGTGATCCCGTAGCGC
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9.4%; Score 316; DB 9; Length 160420;
Best Local Similarity 100.0%; Pred. No. 1.7e-172;
Matches 316; Conservative 0; Mismatches 0; Indels 0;
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7283: gap ...
121861: contig of 42.0 ...
21961: gap of 100 bp
124258: contig of 2297 bp in length
100 bp
100 bp 100 contig
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                                                                                                         92924: gap of 100 bp
95822: contig of 2898 bp in length
                                                                                                                                              contig of 2208 bp in length
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contig of 2678 bp in 100 bp 1.
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fragment_chain:2"
22949. 28090
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26191. 28215
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44246. .5165
/note="assembly_fragment:00989
fragment_chain:4"
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ragment_chain:1
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note="assembly_fragment:00095
ragment_chain:1"
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ragment_chain:1"
                                    gap of 100 bp
51: contig of 4543 bp
gap of 100 bp
24: contig of 2863 bp
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fragment_chain:5"
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13358 133457; gap of 100 bp
133458 136357; contig of 2900 bp
Location/Qualifiers
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ragment_chain:5"
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                       contig of
                                                                         61: gap of
92824: contig
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/clone="RP11-83B5"
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                                                                                                                                    gap of 98130:
     gap of
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                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 58, 2000 this sequence version replaced g1:9863622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 114775 bases at least Q40 Consensus quality: 12431 bases at least Q30 Consensus quality: 128697 bases at least Q20 Insert size: 133157; sum-of-contigs Quality coverage: 2.20x in Q20 bases; sum-of-contigs
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15: contig of 10183 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 5425: contig of 5425 bp in length
5426 5525: gap of 100 bp
5526 9483: contig of 3958 bp in length
9484 9583: gap of 100 bp
9584 14280: contig of 4697 bp in length
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5436 bp in length
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5715 bp in length
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2542 bp in length
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3119 bp in length
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f 2025 bp in length
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contig of 8920 bp in length
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contig of 2658 bp in length
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69094: contig of 3009 bp in length
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82943: contig of 2134 bp in length
                                                                                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                          site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                     Summary Statistics
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28215: contig of
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Direct Submission
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SOURCE
ORGANISM
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JOURNAL
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                                                                                            AUTHORS
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496 bp DNA linear STS 30-MAR-2000 SHGC-83858 Human Homo sapiens STS genomic, sequence tagged site. G50805
G50805.1 GI:5221982
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 496) Olivier, M. and Cox, D.R. Unpublished, Olivier, M., Cox, D.R. (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC ends sequenced at TIGR from the RPC111 BAC library. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
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21 GGAATTCCCCTTGGATTCATTTTCAACCCAACAGGAAGTGAAGGCAAGAGAATCCAAGAGGGTT 80
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for 30 seconds
for 30 seconds
for 23 seconds
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each 200 uM
0.07 units/ul
5 ul
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94 degrees C for 30
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Perkin Elmer 9700
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Local Similarity 100.0%; Pred. No. 9.2e-28;
les 69; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA
Tel: (650) 320-5800
Fax: (650) 320-5801
Fmax: (650) 320-5801
Primer A: TGCTCTTAAAATTGCTCCCTTGA
Primer B: AAATGAGGCTCAGAGAGTGTGG
STS size: 348
PCR Profile:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="10"
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132 . 479
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Annealing:
Polymerization:
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Thermal Cycler:
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a 27571 c 27577 g 39953 t 3212 others
                                                                                                                                                                                                                                                                     77426. 80709

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109144. .112146
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117284. .121861
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F243081SO3 1728 bp DNA linear PRI 13-JUN-2001
Homo sapiens intrinsic factor-vitamin B12 receptor (CUBN) gene,
exons 5 and 6.
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1 (bases 1 to 1728)
Aminoff, M., Brady, S., Verroust, P.J., Moestrup, S.K. and Krahe, R.

The genomic structure of the human CUBN gene encoding cubilin, the intrinsic factor-vitamin B12 receptor
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Submitted (08-MAR-2000) Division of Human Cancer Genetics, Ohio
State University, 420 West 12th Avenue, Columbus, OH 43210, USA
Location/Qualiflers
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Aminoff, M., Brady, S., Verroust, P.J., Moestrup, S.K. and Krahe, R.
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36018...40547
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40648...51635
/note="assembly_name:Contigl3"
51736...87131
/note="assembly_name:Contigl5"
47032...153364
/note="assembly_name:Contigl6"
153465...154748
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Pred. No. 2.4e-05;
                                                                                                          1302. .4039
/note="assembly_name:Contigl1
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/note="assembly_name:Contig14
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100.0%; Pred. No.
0; Mismatches
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Db 95867 GTTCCACTCATCTGGAATTCCCCTTGGA 95897
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125. .226
/gene="CUBN"
                                                 /db_xref="taxon:10090"
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/clone="RP24-354K9"
Location/Qualifiers
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/gene="CUBN"
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Best Local Similarity 100.
Matches 31; Conservative
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Homo sapiens.
Homo sapiens
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                                                     AC125150 154748 bp DNA linear HTG 26-JUN-2002
Mus musculus chromosome UNK clone RP24-354K9, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 154748) MCPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 154748) Meterston, F. H. McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pleces aris not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 8.91 in Q20 bases; agarose-fp Quality coverage: 8.71 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13: 0%
Sequencing vector: M13: 0%
Sequencing vector: plasmid: 100%
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990319
Consensus quality: 151541 bases at least 040
Consensus quality: 151209 bases at least 030
Consensus quality: 152209 bases at least 020
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35917: contig of 31778 bp in length
36017: gap of unknown length
40647: contig of 4530 bp in length
40647: gap of unknown length
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of 66133 bp in length
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of 35396 bp in length
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of 2738 bp in length
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of 1284 bp in length
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AC122150.1 GI:21490651
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Insert size: 154048; sum-of-contigs
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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Kozyraki, R., Verroust, P.J. and Krahe, R.
Direct Submission
Submitted (25-NOV-1998) Medical Biochemistry, University of Aarhus,
Ole Worms Alle, Aarhus 8000 C, Denmark
Sequence update by submitter
On Nov 30, 1998 this sequence version replaced gi:3172328.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Barn H., Verroust, P.J., Nexo, E., Hager, H., Jacobsen, C.,
Christensen, E.I. and Moestrup, S.K.
Characterization of an epithelial approximately 460-kDa protein
that facilitates endocytosis of intrinsic factor-vitamin B12 and
binds receptor-associated protein
J. Biol. Chem. 272 (42), 26497-26504 (1997)
                                                                           Gaps
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Moestrup,S.K., Kristiansen,M., Kozyraki,R., Tommerup,N. and
Verroust,P.J.
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                                  Length 1728;
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0.7%; Scor.
100.0%; Pred. No. v.v.
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/chromosome="10"
/map="10p12"
27. .10898
                                                                                                          1236 CTGCCAGAATGGAGGCACATGTGTT 1260
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QWKGPLCSADVNECELYSGTPLSCQNGGTCVNTMGSYSCHCPPETYGPQCASKYDDCE GGSVARCVHGICEDLMREQAGEPKYSCVCDAGWMSSPNSPACTLDRDECSFQPGPCST LVQCFNTQGSFYCGACPTGWQGNGYICEDINECEINNGGCSVAPPVECVNTPGSSHCQ PQGEQIQINFTHVELQCQSDSSQNYIEVRDGETLLGKVCGNGTISHIKSITNSVMIRF KIDASVEKASFRAVYQVACGDELTGEGVIRSPFFPNVYPGERTCRWTIHQPQSQVILL NFTVFEIGSSAHCETDYVEIGSSSILGSPENKKYCGTDIPSFITSVYNFVKSS STENHGFMAKFSAEDLACGEILTESTGTIQSPGHPNVYPHGINCTWHILVQPNHLIHL **HFTNFSLEEAIGNYYTDFLEIRDGGYEKSPLLGIFYGSNLPPTIISHSNKLWLKFKSD** QIDTRSGFSAYWDGSSTGCGGNLTTSSGTFISPNYPMPYYHSSECYWWLKSSHGSAFE ?QATFMKIFGNDNIVGTHGKVASPFWPENYPHNSNYQWTVNVNASHVVHGRILEMDIE PNVKSSNNSMLLVFKTDSFQTAKGWKMSFRQTLGPQQGCGGYLTGSNNTFASPDSDSN GMYDKNLNCVWIIIAPVNKVIHLTFNTFALEAASTRQRCLYDYVKLYDGDSENANLAG GKYCGTLLPNPVFSQNNELYLRFKSDSVTSDRGYE1 IWTSSPSGCGGTLYGDRGSFTS PGYPGTYPNNTYCEWVLVAPAGRLYTINFYFISIDDPGDCVQNYLTLYDGPNASSPSS GPYCGGDTSIAPFVASSNQVFIKFHADYARRPSAFRLTWDS" **HFHSDSQISDQGFHITYLTSPSDLRCGGNYTDPEGELFLPELSGPFTHTRQCVYMMKQ** RITAPEGRRITLMFNNLRLATHPSCNNEHVIVFNGIRSNSPQLEKLCSSVNVSNEIKS putative 'note='

99. 10895 /product-intrinsic factor-B12 receptor" 120. 131 /note="encodes recognition sequence for furin-mediated

423. .536 /note="encodes EGF r. 537. .665

cleavage

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147280 bp DNA linear PRI 24-APR-2002
AC067747
AC067747, GI:20279381
                                                                                                                                                                                                                                                                                      Submitted (27-APR-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA (bases 1 to 147280)
                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (20-FEB-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
4 (bases 1 to 147280)
Smith, D.R.
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                                                                                                                                            Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147280)
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Bantsni,J., Blimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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HTG; HTGS_PHASE1.
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Smith, D.R.
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100.0%; Pred. No. 0.069;
Live 0; Mismatches 0; Indels
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/note="encodes CUB domain"
7734. 8090
/note="encodes CUB domain"
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/note="encodes CUB domain" 9858. .10208
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/note="encodes CUB domain"
10209. .10556
/note="encodes CUB domain"
10557. .10895
'note="encodes EGF repeat"
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/note="encodes CUB domain"
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8784. .9134
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9135. 9494
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/note="encodes EGF r
1446. .1793
/note="encodes CUB d
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note="encodes CUB
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/note="encodes E
1222. .1322
/note="encodes E
                                   816. .944
/note="encodes
          566. .815
/note="encodes
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Submitted (30-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 152895)
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Submitted (18-UGL-2002) Human Genome Sequencing Center, Department
Modecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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On Jul 14, 2002 this sequence version replaced gi:20340380.
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 91714 bases at least Q40
Consensus quality: 98583 bases at least Q30
Consensus quality: 103878 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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Location/Qualifiers
1. 789
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Partial sequence of EGF-11ke repeat domain of human Notch2 mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Direct Submission
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (11-JUJ-1994) M.T. Lardelli, Karolinska Institute,
Submitted (11-JUJ-1994) M.T. Lardelli, Karolinska Institute,
Developmental Biology Laboratory, CMB, 171 77 Stockholm, SWEDEN
2 (bases 1 to 622)
Larsson,C., Lardelli,M., White,I. and Lendahl,U.
The human NOTCHI, 2, and 3 genes are located at chromosome positions 9934, 1p13-p11, and 19p13.2-p13.1 in regions of neoplasia-associated translocation
Genomics 24 (2), 253-258 (1994)
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100.0%; Pred. No. 0.078;
.ive 0; Mismatches 0; Indels 0
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                                                                                    contig of 1754 bp in length
gap of unknown length
contig of 4225 bp in length
gap of unknown length
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of 5673 bp in length
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of 6597 bp in length
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unknown length
of 4470 bp in length
                                                                                                                                                                                                                                                                                                  gap of unknown length
contig of 7271 bp in length
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of 5812 bp in length
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Best Local Similarity 100.
Matches 25; Conservative
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Matches

ò QΩ ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL

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/translation="MVNSCCGSVCSDQCGLENCCRPSYCQTTCCRTTCCRPSCCVSS CCRPQCCQTTCCRTTCCRTTCCR PSCCRPQCCQSTCCRTTCCR PSCCRPQCCQSYCCQPTCCRTTCCRPTCCRPTCCRPTCCRPQCCQSVCCQPTCCCPSYCVSPCTRPCCRPQCCQTTCCRTTCCRPCCVSRCYRPHC
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                  Rogers, M.A., Langbein, L., Winter, H., Ehmann, C., Korn, B. and Schweizer, J. Characterization of a cluster of human high/ultrahigh keratin associated proteins on chromosome 17q12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human homologs of a Drosophila Enhancer of split gene product define a novel family of nuclear proteins

Nat. Genet. 2 (2), 119-127 (1992)

1303260
                                                                                                                                                           Direct Submission
Submitted (16-OCT-2000) Rogers M.A., Research Program B, Gerr
Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg,
Germany 69120, GERMANY
Related genomic sequence: AC006070 (146419-146919nt).
Location/Qualifiers
1. 1099
/organism="Homo sapiens"
/ob_xref="taxon:9606"
/chromosome="17"
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HOMO Sapiens NOTCH 2 (N2) mRNA, complete cds.
AF308601 M99437
AF308601.1 GI:11275977
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Blaumueller,C.M. and Mann,R.S.
Complete Human Notch 2 (hN2) cDNA sequence
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Blaumueller, C.M. and Artavanis-Tsakonas, S.
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0.91;
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/standard_name="KAP4.4"
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/protein_id="CAC27575.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.7%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:12655446"
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/clone="sc123"
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365 c
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    (bases 1 to 1099)
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Homo sapiens mRNA for keratin associated protein (KRTAP4.13 gene).
AJ296168
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Homo sapiens mRNA for keratin associated protein 4.4 (KRTAP4.4
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 924)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-OCT-2000) Rogers M.A., Research Program B, German
Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                      Characterization of a cluster of human high/ ultrahigh keratin associated proteins on chromosome 17q12-21 Unpublished
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  Indels
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/protein_id="CAC27563.1"
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AJ406936.1 GI:12655445
Keratin associated protein 4.4; KRTAP4.4 gene.
                                                                                                                                                                                                                                                            keratin associated protein; KRTAP4.13 gene.
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Mismatches
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/db_xref="taxon:9606"
/chromosome="17"
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Location/Qualifiers
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/gene="KRTAP4.13"
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                                                      682 CAGCCCTGCCAGAATGGAGGCAC 704
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Rogers, M.A.
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nes 23; Conservative
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PRI 22-NOV-2000

LOCUS

RESULT 13 HSA406936 ACCESSION

BASE COUNT

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/gene="N2"

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AR102329
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TITLE
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SOURCE
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                         Submitted (27-APR-1993) Boyer Center for Molecular Medicine, Howard Hughes Medical Institute, 295 Congress Ave., New Haven, CT 06519,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVNGYQCNCQPGTSGYNCETNFDDCASNPCTHGTCMDGTNRYSCYCSPGFTGQRCNTD
TDECASNPCRKGATCTNGVNGFRCTCPBGPHHPSCYSQVNECLSNPCTHGNCTGGLSG
YKCLCDAGWYGTNCEVDKNECLSNPCQNGGTCDNLVNGYRCTCKKGFKGYNCQVNTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTCLCAPGWGGQRCTIDIDECISKPCMNHGLCHNTQGSYMCECPPGFSGMDCEEDIDD
CLANPCQNGGSCMDGVNTFSCLCLPGFTGDKCQTDMNECLSEPCKNGGTCSDYVNSYT
CKCQAGFDGVHCENNINECTESSCFNGGTCVDGINSPSCLCPVGFTGSFCLHEINECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSENIDDCAFASCTPGSTCIDRVASFSCMCPEGKAGLL/CHLDDACISNPCHKGALCDT
NPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFHCECLKGYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CVDKVNRFQCLCPPGFTGPVCQIDIDDCSSTPCLNGAKCIDHPNGYECQCATGFTGVL
CEENIDNCDPDPCHHGQCQDGIDSYTCICNPGYMGAICSDQIDECYSSPCLNDGRCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASNPCLNQGTCFDDISGYTCHCVLPYTGKNCQTVLAPCSPNPCENAAVCKESPNFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPCLNEGTCVDGLGTYRCSCPLGYTGKNCQTLVNLCSRSPCKNKGTCVQKKAESQCL
CPSGWAGAYCDVPNVSCDIAASRRGVLVEHLCQHSGVCINAGNTHYCQCPLGYTGSYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEQLDECASNPCQHGATCSDFIGGYRCECVPGYQGVNCEYEVDECQNQPCQNGGTCID
LVNHFKCSCPPGTRGLLCEENIDDCARGPHCLNGGQCMDRIGGYSCRCLPGFAGERCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSPCQHGGSCHPQRQPPYYSCQCAPPFSGSRCELYTAPPSTPPATCLSQYCADKARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVCDEACNSHACQWDGGDCSLTMENPWANCSSPLPCWDYINNQCDELCNTVECLFDNF
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MPPEQLLQDARSFLRALGTLLHTNLRIKRDSQGELMVYPYGYGEKSAAMKKQRMTRRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MPALRPALLWALLALWLCCAAPAHALQCRDGYEPCVNEGMCVTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INGTGYCKCPEGFLGEYCQHRDPCEKNRCQNGGTCVAQAMLGKATCRCASGFTGEDCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :VANQFSCKCLTGFTGQKCETDVNECDIPGHCQHGGTCLNLPGSYQCQCPQGFTGQYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGVNTYNCRCPPQWTGQFCTEDVDECLLQPNACQNGGTCANRNGGYGCVCVNGWSGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRCEMD I NECHSDPCQNDATCLDK I GGFTCLCMPGFKGVHCELE I NECQSNPCVNNGQ
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VASNMPDGFICRCPPGFSGARCQSSCGQVKCRKGEQCVHTASGPRCFCPSPRDCESGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGEQEQEVAGSKVFLEIDNRQCVQDSDHCFKNTDAAAALLASHAIQGTLSYPLVSVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSLYVPCAPSPCVNGGTCRQTGDFTFECNCLPGFEGSTCERNIDDCPNHRCQNGGVC
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Blaumueller,C.M. and Mann,R.S.

Blaumueller,C.M. and Mann,R.S.

Blaumueller,C.M. and Mann,R.S.

Submitted (15-NOV-2000) Developmental Biology and Cancer,

Submitted (15-NOV-2000) Developmental Biology and Cancer,

Massachusetts General Hospital Cancer Center, Building 149, 13th

Street, Charlestown, MA 02129-2000, USA

Sequence update by submitter

Sequence version replaced gi:189263.
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1. .9722
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   Direct Submission
Submitted (27-APR
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AUTHORS
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COMMENT
FEATURES
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misc_feature

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                                                                                                                                                                                                                                                                                                                     Gaps.
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                                                                                    /note="Region: transmembrane domain"
449. .6525
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                                                                                                                                                                                /note="Region: CDC10/ANK repeats"
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5050. .5124
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                                                                                                                                                                                                                           /note="Region: PEST domain"
2518 c 2451 g 2491 t
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Sequence 21 from patent US 6083904.
AR102329
AR102329.1 GI:12813127
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                                                                                                                                                                                                                                                                                    0.7%; Score 23; DB
100.0%; Pred. No. 1;
Live 0; Mismatches
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100.0%; Pre
0;
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                                                                                                                                                5482. .6123
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                                                                                                                                                                                              7171. .7356
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                           /gene="N2
                                                                                                                                                                                                                                                                                      Query Match 0.79
Best Local Similarity 100.(
Matches 23; Conservative
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23 0.7 6728 24 AAD28942 Human MOL1D	23 0.7 7410 24	22 0.7 1851 22 AAK53119 Human polytrocleot	20 0.6 972 23 AAS64374 ENA en	20 0.6 1503 24 ABL91801 20 0.6 1755 20 AAX85838	18 20 0.6 2565 19 AAV41622 Nucleotide sequenc 19 20 0.6 2565 21 AAA96940 cDNA encoding LIPG	20 0.6 2802 24 ABL39928	22 20 0.6 4282 21	20 0.6 4352 22 AAI58667	20 0.6 14775 23 ABL17452	26 20 0.6 39328 24 ABL91800	2/ 19 0.6 123 22 ABA/4045 28 19 0.6 123 22 AAK22499	19 0.6 123 22 AAK48667	31 19 0.6 123 24 ABS22406 Human	32 19 0.6 250 21 AAC24350	33 19 0.0 469 23 ABL2394/ 34 19 0.6 505 22 ABA61547	35 19 0.6 505 22 AAK09848	37 19 0.6 505 22 AAI41457	19 0.6 505 24 ABS10004	40 19 0.6 1272 20 AAX61296 Yeast	19 0.6 1320 22 AAH53507 S 19 0.6 1329 21 AAC43184 A	19 0.6 1329 21 AAC49986 Arabidopsis .	19 0.6 1509 23 AAS89522		ALIGNMENTS		RESULT 1 ABK92207	ID ABK92207 standard; DNA; 3375 BP.	AC ABK92207;	XX XX DT 15-AUG-2002 (first outro)		DE Prostate cancer-associated DNA sequence #93. XX	KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;	dense circums and	OS Mammalia. XX	PN W0200230268-A2.	XX PD 18-APR-2002.	12-0cm-2001 : 2001w0-m23204	12-OCT-2001;	PR 13-OCT-2000; 2000US-0687576.	08-DEC-2000;	24-JAN-2001; 16-MAR-2001;	16-MAR-2001;	24-APR-2001;	30-APR-2001;	1007 - IVW - 50
	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Communen Ltd		OM nucleic - nucleic search, using sw model	Run on: May 5, 2003, 04:05:09 ; Search time 464 Seconds	(without alignments) 16380.376 Million cell updates/sec		ct score: 3375	Sequence: 1 gacagigiticgcggctgcactgiccaccttgaaggictic 3375		Gapop 60.0 , Gapext 60.0	Searched: 2185239 segs, 1125999159 residues			Total number of hits satisfying chosen parameters: 4370478	DB seg length:	Maximum DB seq length: 200000000	Post-processing: Listing first 45 summaries	Database : N Geneser 101002.*		<pre>/> /SIDSZ/gcgdata/geneseqn-emb1/NA1981.DAT:* 3: /SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*</pre>	4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:* 5: /SIDS2/gcgdata/geneseqn/geneseqn-embl/NA1984_DAT:*	6: /SIDS2/gcgdata/geneseq/genesequemus/wal961941.bft.* 7: /STDS2/gcgdata/geneseq/genesequemus/wal961941.*	. />LDSZ/gcgdata/geneseq/geneseqf=emb1/NA1987.DAT:* 8: /S1DSZ/gcgdata/geneseqre-emb1/NA1987.DAT:*	9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*	10: /siDSz/gcgdata/geneseq/genesegn-embl/NA1969.DAT:* 11: /SIDSz/gcgdata/geneseq/genesegn-embl/NA1990.DAT:*	12: /SIDS2/gcgdata/geneseq/genesegn-embl/Na1991.DAT:* 13: /SIDS2/gcgdata/geneseg/genesegn-embl/Na1992.DAT:*	14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:	15: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*	11. /S1DS2//orgadata/genesseq/qenesseqn-embl/NAL94b.DAT:* 18. /S1DS2/orgdata/genesseq/deneseqn-embl/NAI997 DAT:*	19: /SIDS2/gcgdata/geneseq_/yeneseqn-emb1/Na1998.DAT:*	20: /SIDS2/gcgdata/geneseq/geneseqn-embl/Na1999.DAT:* 21: /SIDS2/gcgdata/geneseg/genesegn-embl/Na2000.DAT:*	22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001a.DAT:*	24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*	Pred. No. is the number of results predicted by chance to have a	greater than on equal to the score of the result being pr	and is derived by analysis of the total score distribution.	SUMMARIES	Result Query	No. Score Match Length DB ID Description	3375 100.0 3375 24 ABK92207 Prostate	537 45.5 3485 23 AASB1530 296 8.8 406 23 AASB1529	32 0.9 1837 21 AAZ61803 CDN	32 0.9 1837 24 ABL34888	25 0.7 1422 23 AAS92463	23 0.7 394 21 AAC05374

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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various or are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various or prostate cancer and are derived from the tissues of various or aganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing or treating prostate cancer. as well as for useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit in gene therapy, as a vaccine or in antisense applications.

ARK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                               Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes
                                               Hevezi
                                               Afar D,
                                                                                                                                                                                                                                                                                    Claim 22; Page 376-377; 436pp; English.
                                                                                                                                                                                                                                       tissue
                                               Wilson KE,
                                                                                                                                                                                                                                       are expressed in a prostate
BIOTECHNOLOGY
                                                                                         2002-471335/50
                                               Mack DH,
                                                                                                                  P-PSDB; ABG61891
EOS
                                            Gish KC,
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Sequence 3375 BP; 660 A; 944 C; 1062 G; 709 T; 0 other;

ö 120 0; Gaps 240 300 360 420 420 480 540 61 TITTATITGCAGACCTGGGCCGATGCCGCTTTAAAAAACGCGAGGGGCTCTATGCACCTC 120 CCCCCTGGCCCGAGCCGCGCCCGGGTCTGTGAGTAGAGCCGCCGGGGCACCGAGCGCTGG 300 360 9 . 09 1 GACAGTGTTCGCGGCTGCACCGCTCGGAGGCTGGTGACCCGCGTAGAAGTGAAGTTACTT GACAGTGTTCGCGGCTGCACCGCTCGGAGGCTGGGTGACCCGCGTAGAAGTGAAGTACTT ACAAACAGGTGTCCCACGTGGCAGCCGCGCCCCCGGGCGCCCCTGTGTGATCCCGTAGCG TCGCCGCTCTCCCTTCCGTTATATATCAACATGCCCCCTTTCCTGTTGCTGGAGGCCGTCTGT GAAACCATCGGGAAGATTTCAGCTGCCAGCAAAATGATGTGGTGCTCGGCTGCAGTGGAC **ATCATGTTTCTGTTAGATGGGTCTAACAGCGTCGGGAAAGGGGAGCTTTGAAAGGTCCAAG** Length 3375; Indels 24; ö DB 100.0%; Score 3375; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Similarity tches 3375; Query Match Local 181 241 361 481 301 481 301 361 421 g g qq g 9. Q ò ò ò g ò ò 요 ŏ g ò

1380 GCCGTGCTGAGCGAGGACTCTCGGGCCCGAGTGGGTGTGGCCACATACAGCAGGAGCTG 1500 840 840 960 999 9 780 780 900 CACTTTGCCATCACAGTCTGTGACGGTCTGGGACATCAGCCCCGAGAGGGTCAGAGTGGGA GCATTCCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAA CAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGGAGACGGAA CAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGCGCACGGAGACGGAA CTTGCTCTGAAATACCTTCTGCACAGAGGTTGCCTGGAGGCAGAAATGCTTCTGTGCCC CAGATCCTCATCATCGTCACTGATGGGAAGTCCCAGGGGGATGTGGCACTGCCATCCAAG CAGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGTGGGGGTCAGGTTTCCCAGGTGGGAG 841 CAGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGTGGGGGTCAGGTTTCCCAGGTGGGAG GAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCAGCACGTGCTGTTGGCTGAGCAGGTG ACCCCAGACTGCAGGGTCGAGGCTCACCCCTGTGAGCACAGGACGCTGGAGATGGTCCGG GAGTTCGCTGGCAATGCCCCATGCTGGAGAGCATCGCGGCGGGACCCTTGCGGTGCTGGCT GCACACTGTCCCTTCTACAGCTGGAAGAGTGTTCCTAACCCACCTGCCACCTGCTAC CCAGAAGGACTGGACGGCTACCAGTGCCTCTGCCCGCTGGCCTTTGGAGGGGAGGCTAAC GCGGGCACCACTCTGGACGGCTTCCTGCGGGCCAAAGTCTTCGTGAAGCGGTTTGTGCGG CTGGTGGCGGTGCCTGTGGGGGAGTACCAGGATGTGCCTGACCTGGTCTGGAGCCTCGAT GCATTCCAGTTCAGTTCCACTCCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAA GAGGATGCCACCAACGGCCTCTTCAGCACCCTCAGCAGCTCGGCCATCTGCTCCAGCGCC AGGACCACCTGCCCAGGCCCCTGTGACTCGCAGCCCTGCCAGAATGGAGGCACATGTGTT 1201 781 841 961 1021 1021 1081 1081 1141 1141 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1561 1561 601 661 661 721 721 781 901 901 961 1501 541 601 g g g q g a g g g g g qq q g q g ò ò ò ò ò ð ò ò ò ò ò õ ò ò ò

	-F 0-0 0-0 4-	D9 3021 AGGCCTTTACTAGAGCATCCTTTGGAC QY 3121 GCAGCTTTTCCACTTCCCCAGAGACAC Db 3121 GCAGCTTTTCCACTTCCCCAGAGACAC QY 3181 CTTGAGGGACGTTTGTGACTTCTGG	Oy 3241 GGTCTCAGACTGAATGTGACCAATTAA	3361 SULT 2 S81530 AAS81 AAS81 13-FE	AA DNA encoding novel human diagnos XX XX KW Human; chromosome mapping; gene XW food supplement; medical imaging XX OS Homo sapiens. XX NO200175067-A2.	11-OCT-2001, 30-MAR-2001; 31-MAR-2000; 23-AUG-2000; (HYSE-) HYSEQ
<u> </u>		· · · · · · · · · · · · · · · · · · ·		<u> </u>		·
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1621 CGTGGCTTCGGGA 1621 CGTGGCTTCGGGA 1681 CTCACTGAGTCAC 1681 CTCACTGAGTCAC 1741 GAGCTGCTCCTGC 1741 GAGCTGCTCTGC 1741 GAGCTGCTCTGC 1741 GAGCTGCTCTGC 1741 GAGCTGCTCCTGC 1741 GAGCTGCTCCTGC 1801 GGCAGCCCAAAGC	1861 GAGCCCAAAGCATGTGCTACTACGGATCCTCAGGATCTGTTCAACCACATACTACTACTACTACTACTACTACTACTAC	1981 AGCTTTGTGAAGCTGGCCCTCCAGTTGAGCTGAACCTGACGTGACCAGGTGGGC 2041 CTGGTGGTGATGGCAGCCAGCTGAGCTTGGGCTGGACCTGACGTGGCCCCGG 2041 CTGGTGGTGATGGCAGCCAGCGTGCCTTCGGGCTGGACACCAAACCCACCGG 2041 CTGGTGGTGTTGTTTTTTTTTTTTTTTTTTTTTTTTTT	11	2281 GCCGAGAAGATGATTCTCTTGGTGGGTGGGGGGGGGGGG	2461 2461 2521 2521	2581 TGGAGCTCTTGCTGTATGTGTGAGCCAGGATTCTTGAGACGCCCCTGAGGCAC 2640 [11111111111111111111111111111111111
		4 6 6 6			40 60 60 60 60 60 60 60 60 60 60 60 60 60	oy oy oy

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polypeptide (II) sequences: (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The care also used in diagnostics as expressed sequence tags to restore normal activity of (II) is useful in gene therapy techniques (C restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and contain sequences of the invention of diagnostic coding sequences of the invention of diagnostic product data for this patent did not appear in the printed contain the printed contains the printed contains
                                                                                                                                                                                                     useful in
of mutations
                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to isolated polynucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                       ID No 17334; 103pp; English
                                                                                                                                                                                                     isolated polynucleotide and
                                   ΰ
                                   Liu
                                                                                                                                     P-PSDB; ABG17343
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                                   RT,
                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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Ouery Match

Query Match

Query Match

A5.5%; Score 1537; DB 23; Length 3485;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps

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1334 1394 2128 1454 2188 1514 TGTGGGGGAGTACCAGGATGTGCCTGACCTGGTCTGGAGCCTCGATGGCATTCCCTTCCG 1574 2308 2428 AGGCCCCTGTGACTCGCAGCCCTGCCAGAATGGAGGCACATGTGTTCCAGAAGGACTGGA 1274 1949 AGGCCCCTGTGACTCGCAGCCCTGCCAGAATGGAGGCACATGTGTTCCAGAAGGACTGGA GAGCCTGGAATGCAGGTCGACCTCCTCTTCCTGCTGGACAGCTCTGCGGGGCACCACTCT TGGTGGCCCCACCCTGACGGCAGTGCCTTGCGGCAGGCGGCAGAGCGTGGCTTCGGGAG CGGCTACCAGTGCCTCTGCCCGCTGGCCTTTGGAGGGGAGGCTAACTGTGCCCTGAAGCT CGGCTACCAGTGCCTCTGCCCGCTGGCCTTTGGAGGGGAGGCTAACTGTGCCCTGAAGCT GAGCCTGGAATGCAGGGTCGACCTCCTCTTCCTGGACAGCTCTGCGGGCACCACTCT GGACGGCTTCCTGCGGGCCAAAGTCTTCGTGAAGCGGTTTTGTGCGGGCCGTGCTGAGCGA GGACTCTCGGGCCCGAGTGGGTGTGGCCACATACAGCAGGGAGCTGCTGGTGGCGGTGCC 1215 1275 2009 1335 2069 1395 2129 1455 1515 1575 2309 1635 2369 2189 අ ò ŏ Db δy g g δ οχ q δ g δ g à

CTCCGAGGATGAGGTTGCGGCCCAGCGCGTCACGCAAGGGCGCGAGAGCTGCTCCTGCT 2969 GGTGGTGCTCACAGGCGGGAGAGGCGCAGAGGATGCAGCCGTTCCTGCCCAGAAGCTGAG GAGGCTTGCAGGTCCCCGGGATTCCCTGATCCAGTGGCAGCTTACGCCGACCTGCGGTA 3149 CCACCAGGACGTGCTCATTGAGTGGCTGTGTGGGGGAGCCAAGCAGCAGCAGTCAACCTCTG CAAGTGTCGGGATGGCTGGGAGGCCCCCACTGCGAGAACCGTGAGTGGAGCTCTTGCTC 3329 TGTATGTGTGAGCCAGGGATGGATTCTTGAGACGCCCCTGAGGCACATGGCTCCCGTGCA 2429 CTCCGAGGATGAGGTTGCGGGCCCAGCGCGTCACGCAAGGGCGCGAGAGCTGCTCCTGCT GGGTGTAGGCAGTGAGGCCGTGCGGGCAGAGCTGGAGGAGAGCACACAGGCCAAAAGCA 2549 TGTGATGGTCTACTCGGATCCTCAGGATCTGTTCAACCAAATCCCTGAGCTGCAGGGGAA CAGCCAGGTGCAGACTGCCTTCGGGCTGGACACCCAAACCCACCGGGCTGCGATGCTGCG GGCCATTAGCCAGGCCCCTACCTAGGTGGGGTGGGCTCAGCCGGCACCGCCCTGCTGCA GAGGCTTGCAGGTCCCCGGGATTCCCTGATCCACGTGGCAGCTTACGCCGACCTGCGGTA CCACCAGGACGTGCTCATTGAGTGGCTGTGTGGAGAAGCCAAGCAGCCAGTCAACCTCTG CAAGTGTCGGGATGGCTGGGAGGGCCCCCACTGCGAGAACCGTGAGTGGAGCTTTTGCTC GCTGTGCAGCCGGCAGCGCCAGGGTGCCGGACAAGCCCCTGGACCTCGTCTTCATGTT GGACACCTCTGCCTCAGTAGGGCCCGAGAATTTTGCTCAGATGCAGAGCTTTGTGAGAAG CTGTGCCCTCCAGTTTGAGGTGAACCCTGACGTGACACAGGTCGGCCTGGTGTGTATGG CATCTATGACAAAGTGATGACCGTCCAGAGGGGTGCCCGGCCTGGTGTCCCCAAAGCTGT GGTGGTGCTCACAGGCGGGGGGGGGCGCAGAGGTGCAGCCGTTCCTGCCCAGAAGCTGAG 2295 GAACAATGGCATCTCTGTCTTGGTCGTGGGCGTGGGGCCTGTCCTAAGTGAGGGTCTGCG CAAACCCAGCCCGTGCATGAATGAGGGCAGCTGCGTCCTGCAGAATGGGAGCTACCGCTG TGTATGTGTGAGCCAGGGATGGATTCTTGAGACGCCCCTGAGGCACATGGCTCCCGTGCA GGAGGCCAGCAGCCGTACCCCTCCCAGCAACTACAGAAGGCCTGGGCCACTGAAATGGT 3485 GCCTACCTTCTGGAATGTCTGTGCCCCAGGTCCTTAG GCCTACCTTCTGGAATGTCTGTGCCCCAGGTCCTTAG 2489 1935 2669 2729 2849 3209 1695 1815 1995 2055 2909 3029 3089 2415 2475 2535 3269 1755 2789 2115 2175 2235 3449 2355 2595 2655 2715 ద δλ q Ω a ŏ qq δý qq οy g οy g Óγ g Qλ g ò g ò g δ g ζ g ò g ŏ qq δŽ ОР δ g δ qq

2736 TGCCCCAGGTCCTTAGAATGTCTGCTTCCCGCCGTGGCCAGGACCACTATTCTCACTGAG 2795

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes. polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2616 GATTCTTGAGACGCCCCTGAGGCACATGGCTCCCGTGCAGGAGGGCAGCAGCAGCCGTACCCC 2675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    `.
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tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 406 BP; 80 A; 112 C; 107 G; 107 T; 0 other;
                                                                                                                                                      DNA encoding novel human diagnostic protein #17333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 17333; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%; Score 296;
                                    AAS81529 standard; cDNA; 406 BP.
                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631
                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73.
P-PSDB; ABG17342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                            WO200175067-A2.
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
                                                                         AAS81529;
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RESULT 3
AAS81529/c
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2676 TCCCAGCAACTACAGAGGCCTGGGCACTGAAATGGTGCCTACCTTCTGGAATGTCTG 2735

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252 TCCCAGCAACTACAGAGAGAGGCCTGGGCCACTGAAATGGTGCCTACCTTCTGGAATGTCTG 193

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The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocytes stem cells and transit amplifying calls. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate anglogenesis and tumnour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to inhibit binding of HV-1 to leukocytes. The invention may also be used from several mouse, rat or human skin cell types. Sequences derived from several mouse, rat or human skin cell types. Sequences concode from several mouse, rat or human skin cell types. Sequences concode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences Azélé56-26166, Azél186, Azél1802-26181780. Azél8127-2618129 encode proteins with one or more putative
                                     2796 GGAGGAGGATGTCCCAACTGCAGCCATGCTTAGAGACAAGAAAGCAGCTGATGTCAC 2855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murison JG;
192 TGCCCCAGGTCCTTAGAATGTCTGCTTCCCGCCGTGGCCAGGACCACTATTCTCACTGAG 133
                                                                                                                                                                                                                                                                                                                                                                                                              Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell, secreted; transmembrane; inflammation; cancer; neurological disease; anglogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides useful for the treatment of various conditions
                                                           132 GGAGGAGGAGGATCCCCAACTGCAGCCATGCTTAGAGACAGAAAGCAGCTGATGTCAC
                                                                                                                   CDNA encoding murine skin cell secreted protein, SEQ ID NO:350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory; cytostatic; neuroprotective; vulnery; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1837 BP; 370 A; 541 C; 557 G; 369 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 204; 235pp; English.
                                                                                                                                                                                                                                                         AAZ61803 standard; cDNA; 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     including wounds and cancer -
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                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane domains.
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09-NOV-1998;
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Murine cDNA isolated from skin cells SEQ ID NO: 350.
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                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                        2000US-206650P.
2000US-221232P.
                                                                                                                                                                                                                                                                                        24-MAY-2001; 2001WO-NZ00099
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                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-122020/16.
                                                                                                                                                                                                                 WO200190357-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                        24-MAY-2000;
25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                     29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 Watson JD,
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AAS92463
       δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammalian skin cells. The polypeptide is useful for stimulating the keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating anglogenesis, inhibiting anglogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus fluty). It oleukocytes, and treating inflammatory diseases, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kumble KD, 'Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present polynucleotide encodes a polypeptide which is expressed in
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                       nootropic; neuroprofective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
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     Length 1837;
                                                                                                                                                                                                                                                                                                                                            skin cell; cytostatic; antiinflammatory; anti-HIV;
                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligonucleotides for examining expression patterns.
0.9%; Score 32; DB 21; I
100.0%; Pred. No. 9.1e-05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1146 CTGTCCCTTCTACAGCTGGAAGAGAGTGTTCC 1177
                                                                        1146 CTGTCCCTTCTACAGCTGGAAGAGAGTGTTCC 1177
                                                                                           942 CTGTCCCTTCTACAGCTGGAAGAGAGTGTTCC 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 272-273; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                   AAC99736 standard; cDNA; 1837 BP
                                                                                                                                                                                                                                                                                                         Skin cell cDNA, SEQ ID NO: 350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2000; 2000WO-NZ00075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0312283
                                                                                                                                                                                                                                                                       (first entry)
                  Similarity 100.
32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-007495/01.
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Best Local Similarity
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                                                                                                                                                                                                                                                                     08-MAR-2001
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                                                                                                                                                                                                                                    AAC99736;
   Query Match
                      Local
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The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumble KD;
Human; rat; mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vulnerary; immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides encoded by the polynucieotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for modulating immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1837 BP; 370 A; 541 C; 557 G; 369 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel human diagnostic protein #28267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 9.1 Matches 32; Conservative 0; Mismatches
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ABL34888;

RESULT 6
ABL34888
ID ABL3.
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AC ABL3.

Matches

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Tang YT;

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                              WPI; 2001-639362/73.
                                                                                   Drmanac RT, Liu C,
                                                      (HYSE-) HYSEQ INC.
                                                                                                                            P-PSDB; ABG28277
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                                                                                                                                                                                                    biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in capponsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 25; DB 23; Length 1422;
100.0%; Pred. No. 0.21;
tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1422 BP; 368 A; 329 C; 356 G; 369 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #28268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 28267; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1236 CTGCCAGAATGGAGGCACATGTGTT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 CTGCCAGAATGGAGGCACATGTGTT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS92464 standard; cDNA; 11344 BP
                                                                                                               Tang YT;
            30-MAR-2001; 2001WO-US08631.
                                     31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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Best Local Similarity
                                                                                                              Liu C,
                                                                                                                                         WPI; 2001-639362/73
                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                        P-PSDB; ABG28276.
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                                                                                                                                                                                                                               biodiversity
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                                                                                                               Drmanac RT,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I ) is useful as hybridisation probes, polypeptide (II) sequences. (I ) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving can polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the proposible for genetic disorders or other trails to assess blodiversity and to produce other types of data and products dependent on DNA and and anino acid sequences. Asset419-Ass44564 represent novel human DNA and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 25; DB 23; Length 11344;
100.0%; Pred. No. 0.2;
iive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
Claim 1; SEQ ID No 28268; 103pp; English.
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Matches 25; Conserv
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24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetes; chromosomal disorder; albinism; anaemia; psoriasis; scarring; liver cirrhosis; neurodegeneration; osteoarthritis; organ rejection; cerebral thrombosis; hypertension; systemic lupus erythematosus; astima; immunodeficiency; rheumatoid arthritis; ulcer; HIV; human immuno deficiency virus; hepatitis; haemostatic disease; pain; haematopoietic; thrombolytic; thrombocytopaenia; Alzheimer's disease; Parkinson's disease; Huntington's disease; muscular disease; stress; ocular disease; growth disorder; depression; epilepsy; contraceptive; vulnerary; osteopathic; haemostatic; tranquiliser; antidepressant; analgesic; vasotropic; hypotensive; gene therapy; chromosome 1; ss.
                                                                                                                                                                   The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted molecule; MOL1b protein; MOLX; cardiomyopathy; atherosclerosis;
                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product= "Human MOL1b protein"
                                      Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                              Claim 1; SEQ ID 9449; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           expression and secretion vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 CAGCCCTGCCAGAATGGAGGCAC 304
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                                                                WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MOL1b cDNA.
            (GEST ) GENSET
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molecule (MOL) polypeptides, designated MOLX polypeptides (i.e. a MOL protein where X is an integer from 1 to 8). Sequences of the invention are useful for treating or preventing a MOLX-associated disorder in humans. They are useful for treating or preventing cardiomyopathy, atheroscierosis and disorders related to cell signal processing and metabolic pathway modulation. The MOLX antibodies are useful for treating or preventing diabetes and disorders related to cell signal processing and metabolic pathway modulation. MOLX sequences are useful for the treatment or diagnosis of other MOLX-associated disorders, e.g. chromosomal disorders, albinism, anaemia, liver cirrhosis, psoriasis, carring, neurodegeneration, osteoarthritis, organ rejection, cerebral thrombosis, ischaemia, hypertension, systemic lupus erytheratosus, immunedeficiency, HIV (human immuno deficiency virus), viral, bacterial and fungal infections, hepatitis, rheumatoid arthritis, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoietic, thrombolytic, haemostatic diseases, thrombocytopaenia, ulcers, Alzheimer's disease, Parkinson's disease, Hutington's disease, cular disease, muscular diseases, growth disorders, loss of 11bido, stress, depression, pain and epilepsy. They are useful for preventing chemocherapy side effects and as contraceptives. Sequences of the invention are also useful for gene therapy. The present sequence is a coby encoding human Notch-like protein, WOLIb. MOLIb gene is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoing secreted polypeptides, designated MOLX polypeptides, useful for treating a MOLX-associated disorder, e.g. cardiomyopathy, atherosclerosis, diabetes and metabolic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tchernev V, Liu X, Shenoy S, Spytek K, Zerhusen
Taupier RJ, Rastelli L, Grosse WM, Szekeres ES;
Lepley DM, Shen L, Burgess CE, Shimkets RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6728 BP; 1571 A; 1647 C; 1668 G; 1842 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
/product= "Human MOLIb mature protein"
4435..6728
/*tag= e
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Local Similarity 100.0%;
les 23; Conservative 0
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2000US-218622P.
2000US-218992P.
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27-JUL-2000; 2000US-221285P-
14-FEB-2001; 2001US-268734P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-155038/20.
P-PSDB; AAE18208.
                                                                                                                                                       WO200206339-A2
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Patturajan M,
Alsobrook J, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000;
17-JUL-2000;
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Secreted molecule; MOLJa protein; MOLX; cardiomyopathy; atherosclerosis; diabetes; chromosomal disorder; albinism; anaemia; psoriasis; scarring; liver cirrhosis; neurodegeneration; osteoarthritis; organ rejection; cerebral thrombosis; hypertension; systemic lupus erythematosus; asthma; immune disease; ischaemia; immunodeficiency; rheumatoid arthritis; ulcer; HIV; human immuno deficiency virus; hepatitis; haemostatic disease; pain; haematopoletic; thrombolytic; thrombocytopaenia; Alzheimer's disease; pain; harkinson's disease; thrombolytic; thrombocytopaenia; Alzheimer's disease; ocular disease; growth disorder; depression; epilepsy; contraceptive; vulnerary; osteopathic; haemostatic; tranquiliser; antidepressant; analgesic; vasotropic; hypotensive; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tchernev V, Liu X, Shenoy S, Spytek K, Zerhusen B;
Taupier RJ, Rastelli L, Grosse WM, Szekeres ES;
Lepley DM, Shen L, Burgess CE, Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses nucleic acid sequences encoding novel secreted
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/product= "Human MOLla mature protein"
                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human MOL1a protein"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..7410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 9-11; 223pp; English.
               ВР
             AAD28941 standard; cDNA; 7410
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03-JUL-2000; 2000US-215902P.
07-JUL-2000; 2000US-216586P.
07-JUL-2000; 2000US-216586P.
17-JUL-2000; 2000US-21672P.
17-JUL-2000; 2000US-218992P.
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2000US-215856P.
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14-FEB-2001; 2001US-268734P.
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                                                                      (first entry)
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76..7407
/*tag= c
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P-PSDB; AAE18207.
                                                                                                     Human MOL1a cDNA
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Alsobrook J,
                                                                      07 - MAY - 2002
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                                           AAD28941;
AAD28941
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molecule (MCL) polypeptides, designated MOLX polypeptides (i.e. a MOL protein where X is an integer from 1 to 8). Sequences of the invention are useful for treating or preventing a MOLX-associated disorder in humans. They are useful for treating or preventing cardiomyopathy, atherosclerosis and disorders related to cell signal processing and metabolic pathway modulation. The MOLX antibodies are useful for

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treating or preventing diabetes and disorders related to cell signal processing and metabolic pathway modulation. MoIX sequences are useful for the treatment or diagnosis of other MoIX-associated disorders, e.g. chromosomal disorders, albinism, anaemia, liver cirrhosis, psoriasis, scarring, neurodegeneration, osteoarthritis, organ rejection, cerebral trrombosis, ischaemia, hypertension, systemic lupus erythematosus, immune diseases, immunodeficiency, HIV (human immuno deficiency virus), viral, bacterial and fungal infections, hepatitis, rheumatoid arthritis, asthma, collers, Alzheimer's disease, parkinson's disease, Huntington's disease, cullers, Alzheimer's disease, parkinson's disease, Huntington's disease, coular disease, muscular diseases, growth disorders, loss of libido, stress, depression, pain and epilepsy. They are useful for preventing chemotherapy side effects and as contraceptives. Sequences of the invention are also useful for gene therapy. The present sequence is a cDNA encoding human Notch-like protein, MoLla.
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R, Wang 2W;
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                                                                                                                                                                                                                                                                                                                 0.7%; Score 23; DB 24; Length 7410;
                                                                                                                                                                                                                                                                               Sequence 7410 BP; 1691 A; 1989 C; 1983 G; 1747 T; 0 other;
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Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 680.
                                                                                                                                                                                                                                                                                                                                                                                                    3577 CAGCCTGCCAGAATGGAGGCAC 3599
                                                                                                                                                                                                                                                                                                                                                                                 1231 CAGCCCTGCCAGAATGGAGGCAC 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK52135 standard; cDNA; 1851 BP
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Matches 23; Conservative
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27-APR-2000;
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19-JUL-2000;
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15-SEP-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK52135;
                                                                                                                                                                                                                                                                                                                   Query Match
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene-therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IC, Cao Y,
Wang ZW;
                                                                                                                                                                                                                                                                   Score 22; DB 22; Length 1851; Pred. No. 5.7;
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                                                                                                                                                                                                                                    Sequence 1851 BP; 379 A; 558 C; 574 G; 340 T; 0 other;
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100.0%; Pred. No. ...
... 0; Mismatches
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Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 2648.
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                                                                                                                                                                                                                                                                                                                               1190 CCACCTGCTACAGGACCACCTG 1211
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2000US-0560875.
2000US-0598075.
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2000US-0654936
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                                                                                                                                                                                                                                                                                  Local Similarity
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19-JUL-2000;
                                                                                                                                                           inflammation
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                                                                                                                                                                                                                                                                     Query Match
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The invention relates to polynucleotides (AAK51456-AAK53435) and the

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encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymorlectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibeterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
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                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation.
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                                                                                                                                                                                                                                 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                     DB 22; Length 1851; 5.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein cDNA sequence #4.
                                                                                                                                                                                                                                                         were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                     1190 CCACCTGCTACAGGACCACCTG 1211
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Parkinson's diseases and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                125 CCACCTGCTACAGGACCACCTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC59627 standard; cDNA; 498 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000; 2000WO-US06828.
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99US-0169616
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08-DEC-1999;
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AAC59627
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                  the diagnosis, freatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colltis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
                                                                                                                                                                                                                            wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
proteins, antibodies and (ant)agonists are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
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mutations
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                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 20; DB 21; Length 498; 100.0%; Pred. No. 52;
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                                                                                                                                                                                                                                                                                                                                                     Sequence 498 BP; 109 A; 184 C; 93 G; 112 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS64374 standard; cDNA; 972 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                        llarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1829 CGGATCCTCAGGATCTGTTC 1848
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG00187.
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nes 20; Conserv
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nucleic
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                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                    Gaps
polypeptide and polynucleotide sequences have applications in
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                                                                                                                                                                                                                                                                                     DB 23; Length 972;
52;
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                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No.
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100.0%; Pre
0; /
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Matches 20;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

May 5, 2003, 04:59:44; Search time 926 Seconds Run on:

(without alignments)
4306.664 Million cell updates/sec

US-09-930-020A-1 3375 1 gacagtgttcgcggctgcac......tgtccaccttgaaggtcttc 3375 Title: Perfect score: Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

746064 seqs, 590810554 residues

Word size : Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*

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7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Description	Sequence 1, Appli	Sequence 350, App	Sequence 350, App	Sequence 19791, A	Sequence 2842, Ap	Sequence 493, App	Sequence 29368, A	Sequence 5125, Ap	Sequence 12802, A	Sequence 583, App	Sequence 7, Appli	Sequence 14, Appl		Sequence 1005, Ap	Sequence 1005, Ap	Sequence 1125, Ap	Sequence 1125, Ap	Sequence 1125, Ap	Sequence 386, App
	B ID	9 US-09-930-020A-1	9 US-10-152-661-350	9 US-09-866-050A-350	9 US-09-918-995-19791	9 US-09-938-842A-2842	12 US-10-044-090-493	10 US-09-864-761-29368	10 US-09-983-965-5125	10 US-09-864-761-12802	10 US-09-822-849A-583	10 US-09-818-143-7	9 US-10-158-160A-14	10 US-09-805-458A-3	10 US-09-920-300A-1005	12 US-10-033-528-1005	9 US-09-946-807-1125	10 US-09-795-668-1125	10 US-09-795-686-1125	9 US-10-060-036-386
	Query Match Length DB	3375	1837	1837	531	1120	3638	123	297	205	952	3047	32367	172637	384	384	401	401	401	405
æ	Query Match	100.0	6.0	0.9	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	9.0	0.5	0.5	0.5	0.5	0.5	0.5
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Sequence 17637, A Sequence 31656, A Sequence 27118, A Sequence 20362, A Sequence 191, App Sequence 1281, App Sequence 2501, App Sequence 2501, App Sequence 23, Appl Sequence 23, Appl Sequence 25, Appl Sequence 25, Appl Sequence 79, Appl	770000
US-09-918-995-17637 US-09-918-995-11656 US-09-918-995-20118 US-09-918-995-20118 US-09-918-995-20162 US-09-918-995-20657 US-09-918-995-20657 US-09-918-995-1244 US-09-918-995-1244 US-09-918-995-1244 US-09-918-995-1244 US-09-918-995-1244 US-09-918-995-1244 US-09-918-918-918-918-918-918-918-918-918-91	10-245 -10-245 -10-245 -10-237 -10-238 -10-238
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sis of Creening	Score 3375; Pred. No. 0; Mismatches	77666761 7666761
00200A Inc. Diagnos 35 of Sc 57 09/930		rcggagg rcggagg
SULT 1 -09-930-020A-1 -09-930-020A-1 -09-930-020A-1 -09-930-020A-1 -09-930-020A-1 -09-930-020A-1 -09-930-020A-1 -09-930-020A-1 -0-09-930-020A-1 -0-0-9-930-020A-1 -0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-	9,80	SCACCGCT
SULT 1 -09-930-020A-1 -09-930-020A-1 SUBLICALION NO. USZ0030077568A1 GENERAL INFORMATION: APPLICANT: Gish, Kurt C. APPLICANT: Gish, Kurt C. APPLICANT: MACK, David H. APPLICANT: Wilson, Keith E. APPLICANT: EOS Biotechnology TITLE OF INVENTION: Machods of TITLE OF INVENTION: and Method TITLE OF INVENTION: AND METHORS OF INVENTION: AND METHOR FILE OF INVENTION: AND METHOR FILE OF INVENTION: AND METHOR FILING DATE: 2001-08- PRIOR FILING DATE: 2000-09-15 NUMBER: OF SEQ ID NOS: 3 SOGTWARE: PATENTIN VET: 2.1 LENGTH: 3375 TYPE: DAN ORGANISM: HOMO SAPIENS FEATURE: OTHER INFORMATION: CBF9 FEATURE: CCATION: (328). (2751) OTHER INFORMATION: CBF9 FEATURE: OTHER INFORMATION: CBF9 FEATURE: OTHER INFORMATION: CBF9 FOR OTHER INFORMATION: CBF9	, id	GCGGCTC GCGGCTC
APP11: APP11: APP11: APP11: APP11: APP11: G1sh. G1sh. APP11: G1sh. APP11: APP11	simila Simila '5; Cor	AGTGTTC AGTGTTC
RESULT 1 US-09-930-020A-1 Sequence 1, Application Bublication No. US200300 GENERAL INFORMATION: APPLICANT: Gish, Kurt C APPLICANT: Mack, David APPLICANT: Wilson, Kei TITLE OF INVENTION: an TITLE OF INVENTION: an TITLE OF INVENTION: an TITLE OF INVENTION: An FILE REFERENCE: 018901- CURRENT PILICA DATE: 2000 FILE REFERENCE: 10801- CURRENT APPLICATION NUMBE PRIOR APPLICATION NUMBE PRIOR FILING DATE: 2000 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PATENTIN VET. LENGTH: 3375 LENGTH: 3375 LENGTH: 3375 TERATURE: COTHER INFORMATION: CBF FEATURE: NAME,KEX: CDS LOCATION: (328)(2751) CUSTION: GBF COTHER INFORMATION: CBF	Query Match Best Local Similarity Matches 3375; Conserv	1 GAC 1 GAC
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	CTGTGAGTAGAGCCGCCGGGCACCGAGCGCTGG 30	
301	TCGCCGCTCTCCTTCCGTTATATCAACATGCCCCCTTTCCTGTTGCTGGAGGCCGTCTGT 360 	·
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421 (GAAACCATCGGGAAGATTTCAGCTGCCAGCAAATGATGTGGTGCTGGCTG	
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541 (CACTTIGCCAICACAGICIGIGACGGICTGGACAICAGCCCCGAGAGGGICAGAGTGGGA 600 	
601 (GCATTCCAGTTCAGTTCCACCTCATCTGGAATTCCCCTTGGATTCATTTTCAACCCAA 660 	
661 (CAGGAAGTGAAGGCAAGAATCAAGAGGATGGTTTTCAAAGGAGGGGGGCACGGAGACGGAA 720 	
721 0	CTTGCTCTGAAATACCTTCTGCACAGAGGTTGCCTGGAGGCAGAAATGCTTCTGTGCCC 780 	
781 (CAGATCCTCATCATCACTGATGGGAAGTCCCAGGGGGATGTGGCACTGCCATCCAAG 840 	
841 (CAGCTGAAGGAAAGGGGTGTCACTGTGTTTGCTGTGGGGGTCAGGTTTCCCAGGTGGGGG 900 	-
901 (GAGCTGCATGCACTGGCCAGCGAGCCTAGAGGGCAGCAGGTGCTGTTGGCTGAGCAGGTG 960 	
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1141 (GCACACTGTCCCTTCTACAGCTGGAAGAGTGTTCCTAACCCACCTGCCACCTGCTAC 1200 	

1380 2040 2100 2160 2220 2340 1260 1440 1440 1500 1620 1620 1680 1800 1800 1920 1920 1980 2040 2100 2160 CTCACTGAGTCACACTCCGAGGATGAGGTTGCGGGCCCAGCGCGTCACGCAAGGGCGCGA : 1740 GTCCCCAAAGCTGTGGTGGTGCTCACAGGCGGGAGAGGCGCAGAGGATGCAGGCGTTCCT GCCGTGCTGAGCGAGGACTCTCGGGCCCGAGTGGGTGTGGCCACATACAGCAGGGAGCTG CGTGGCTTCGGGAGCGCCACCAGGACAGGCCAGGACCGGCCACGTAGAGTGGTTTTG CTGGTGGCGGTGCCTGTGGGGGAGTACCAGGATGTGCCTGACCTGGTCTGGAGCCTCGAT CGTGGCTTCGGGAGCGCCACCAGGACAGGCCAGGACCGGCCACGTAGAGTGGTTTTG GAGCTGCTCCTGCTGGGTGTAGGCAGTGAGGCCGTGCGGGCAGAGCTGGAGGAGATCACA GGCAGCCCAAAGCATGTGATGGTCTACTCGGATCTCAGGATCTGTTCAACCAAATCCCT GAGCTGCAGGGGAAGCTGTGCAGCCGGCAGGGCCAGGGTGCCGGACACAAGCCCTGGAC GCTGCGATGCTGCGGGCCATTAGCCAGGCCCCCTACCTAGGTGGGGGTGGGCTCAGCCGGC ACCGCCCTGCTGCACATCTATGACAAAGTGACCGTCCAGAGGGGGTGCCCGGCCTGGT GCGGGCACCACTCTGGACGGCTTCCTGCGGGCCAAAGTCTTCGTGAAGCGGTTTGTGCGG 1981 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1501 1561 1561 1621 1621 1681 1681 1741 1801 1801 1861 1861 1921 1921 1981 2041 2041 2101 2101 2161 2161 2221 2221 2281 g g g Q g g g g QQ Dp g g g a g g g ò g ò οχ ò δ ò ò ò à ò ò ò õ Qγ ò δý δ Qγ δ

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APPLICANT: Murisol, James G.
APPLICANT: Murisol, James G.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and methods for Their Use
FILE REFERENCE: 11000.1011c5
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR APPLICATION NUMBER: 09/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-04-29
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APPLICANT: Witson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orust, Rene
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Mumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
CURRENT APPLICANTON NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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100.0%; Pred. No. 1.3
iive 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                           ; Sequence 350, Application US/10152661; Publication No. US20030022835Al; GENERAL INFORMATION:
                                                                                                                                                                                                     Strachan, Lorna
Sleeman, Matthew
  3361 ACCTIGAAGGICTIC 3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 0.9°
Best Local Similarity 100°.
Matches 32; Conservative
                                                                                                                                                                                APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                      Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mouse US-10-152-661-350
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US-09-866-050A-350
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LENGTH: 1837
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GCCGACCTGCGGTACCACCAGGACGTGCTCATTGAGTGGCTGTGTGGAGAAGCCAAGCAG
                                                                                                                                                                           2401 GCCGACCTGCGGTACCACCAGGACGTGCTCATTGAGTGGCTGTGTGGAGAAGCCAAGCAG
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US-09-864-761-29368, Application US/09864761

Sequence 29368, Application US/09864761

Sequence 29368, Application US/09864761

Sequence 29368, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENEE
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGram
SOFTWARE: PERL PROGram
LINGTH: 3638
Gaps
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 400203.1
US-10-044-090-493
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4.2;
   Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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Pred. No.
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                   RESULT 6
US-10-044-090-493
Sequence 493, Application US/10044090
Patent No. US20020137081A1
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Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
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                                                                  2865 ATGTTGTTGAAAAGTTTTGA 2884
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   Conservative
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ORGANISM: Homo sapiens
20;
Matches
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Publication No. US20030073623A1
GENERAL INCORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756;
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 19791
LENGTH: 531
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                    Query Match 0.9%; Score 32; DB 9; Length 1837; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 32; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                             1146 CTGTCCCTTCTACAGCTGGAAGAGAGTGTTCC 1177
                                                                                                                                                                                                                            942 crerccrrcracaccrecaagagagrerrec 973
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Patent No. US20020160378a1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LCCATION: (1)...(531)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-19791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             752 TGCCTGGAGGCAGAATGCT 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 TGCCTGGAGGCAGAAATGCT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-09-918-995-19791/c
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US-09-938-842A-2842
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 12802
LENGTH: 505
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15;
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PRIOR APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PLING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-04
PRIOR PELING DATE: 2000-06-07
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
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100.0%; Pred. No.
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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COTHER INFORMATION: EXPRESSED IN LUNG, S.
COTHER INFORMATION: EXPRESSED IN ADULT L.
COTHER INFORMATION: EXPRESSED IN FETAL L.
COTHER INFORMATION: EXPRESSED IN BRAIN,
COTHER INFORMATION: EXPRESSED IN BONE MA.
US-09-864-761-12802
                                                                                                                                                 RESULT 9
8.09-864-761-12802/c
5. Sequence 12802, Application US/09864761
5. Patent No. US20020048763A1
1488 CAGCAGGGAGCTGCTGGTG 1506
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                                                            38 CAGCAGGAGCTGCTGTG 56
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Best Local Similarity
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NOS: 5912
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PACENTA, SIGNAL = 1.2
OTHER INFORMATION: ATT: AL163218.2, EVALUE 2.00e-63
OTHER INFORMATION: EST_HUMAN HIT: A1807844.1, EVALUE 1.00e-01
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).0%; Pred. No. 16;
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100.0%; Pred. No. 15;
ive 0; Mismatches 0; Indels
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                                            PRIOR APPLICATION NUMBER: PCT/USO1/UU002
PRIOR FILING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00661
PRIOR PELICATION NUMBER: PCT/USO1/00670
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 29368
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APPLICATION NUMBER: PCT/US01/00663
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Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
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Matches 19; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Bos taurus
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US-09-983-965-5125
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RESULT 14
US-09-920-300A-1005/c
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US-09-805-458A-3/c
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Sequence 7. Application US/09818143

Patent No. US2002001900001

GENERAL INFORMATION:

APPLICANT: Walker, Michael G.

APPLICANT: Walker, Mayne

APPLICANT: Klingler, Tod M.

TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES FILE REFERENCE: PB-0004 CIP

CURRENT APPLICATION NUMBER: US/09/818,143

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PERL PROGRAM
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CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR PLING DATE: 2000-04-06
NUMBER OF SED ID NOS: 598
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 15;
ive 0; Mismatches 0; Indels
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15;
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Mismatches
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Pred. No.
                                                                                                                                                        Sequence 583, Application US/09822849A Patent No. US20020045170A1 GENERAL INFORMATION:
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Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
Genetics Institute, Inc.
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100.0%; Pro
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                                 2718 TACCTTCTGGAATGTCTGT 2736
                                                     224 TACCTICTGGAATGTCTGT 206
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.US-09-818-143-7
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Best Local Similarity 100.
Matches 19; Conservative
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Conservative
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                                                                                                                                                                                                                             Clárk, Hilary
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-818-143-7/C
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LENGTH: 3047
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LENGTH: 952
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APPLICANT:
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GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al

TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,

TITLE OF INVENTION: SOLOTATED HUMAN ION CHANNEL PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL000722

CURRENT APPLICATION NUMBER: US/09/805,458A

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 14, Application US/10158160A
Publication No. US20030059805A1
Publication No. US20030059805A1
Publication No. US20030059805A1
APPLICANT: RAPPOLD-HOERBRAND, GUDRUN
APPLICANT: RAO, ERCOLE
TITLE OF INVENTION: HUMAN GROWTH GENE AND SHORT STATURE GENE REGION
FILE REFERENCE: 108351-00004
CURRENT APPLICATION NUMBER: 09/147,699
PRIOR APPLICATION NUMBER: 09/147,699
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13;
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Pred. No. 14;
Mismatches 0
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: PCT/EP97/05355
PRIOR FILING DATE: 1997-09-29
PRIOR APPLICATION NUMBER: 60/027,633
PRIOR FILING DATE: 1996-10-01
PRIOR APPLICATION NUMBER: EP/97100583.0
PRIOR FILING DATE: 1997-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09805458A Patent No. US20020042100A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(172637); OTHER INFORMATION: n = A,T,C or G US-09-805-458A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Sc
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 32367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-158-160A-14
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LENGTH: 172637
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Sequence 1005, Application US/09920300A
Patent No. US20020136728A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Weagher, Madeleine Joy
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1005
LENGTH: 384
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Fatent No. US20020131971A1
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher. Madeleine Joy
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12.26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 384
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100.0%; Pred. No. 54;
Live 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 18; Conservative
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ORGANISM: Homo sapiens
US-09-920-300A-1005
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; ORGANISM: Homo sapiens
US-10-033-528-1005
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Search completed: May Job time : 1316 secs

375 TGGAGGATGCCACCAACG 358

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